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PR 25-AUG-1999; 99US-0150566.
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PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154479.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
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PR 14-OCT-1999; 99US-0159637.
PR 18-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
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PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161320.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

alignment_scores:

Quality: 127.00

Ratio: 5.292

Length:

Gaps:

25
0

Percent Similarity: 96.000 Percent Identity: 96.000

alignment_block:

US-09-198-779B-1 x AAW343921 ..

Align seg 1/1 to: AAW343921 from: 1 to: 392

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160 AGGTTTCATCAAGACCGCGCATACGGCCACTTTGGCCGTGACGACGCCGA 209
    |||||||
362 ArgPheIleLysThrAlaIaIaTyGlyHisPheGlyArgAspAspAlaAs 378
    |||||||
210 CTTCACTCGCGAGGTGGTCAAGCCC 234
    |||||||
378 pPheThrTrpGluValValLysPro 386

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seq_name: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:AAW34540

seq_documentation_block:

ID AAW34540 standard; protein; 394 AA.

AC AAW34540;

XX 26-MAR-1998 (first entry)

XX S-adenosylmethionine synthase 1.

XX S-adenosylmethionine synthase 1; sam1; barley; alkali resistant plant.

OS Hordeum vulgare.

XX JP09313186-A.

XX 09-DEC-1997.

XX 28-MAY-1996; 96JP-0133406.

XX 28-MAY-1996; 96JP-0133406.

XX (NIOC) NIPPON OIL CO LTD.

XX WPI: 1998-080077/08.

DR N-PSDB; AAT99141.

PT S-adenosyl-methionine synthase gene - useful in producing plants resistant to alkaline soil

XX Claim 1; Page 5-6; 13pp; Japanese.

CC This sequence represents the S-adenosylmethionine synthase 1 (sam1) protein. The DNA encoding this sequence may be used in producing plants which are resistant to alkaline soil.

XX Sequence 394 AA;

alignment_scores:

Quality: 127.00 Length: 25
Ratio: 5.292 Gaps: 0
Percent Similarity: 96.000 Percent Identity: 96.000

alignment_block:

US-09-198-779B-1 x AAW34540 ..

Align seg 1/1 to: AAW34540 from: 1 to: 394

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160 AGGTTTCATCAAGACCGCGCATACGGCCACTTTGGCCGTGACGACGCCGA 209
    |||||||
362 ArgPheIleLysThrAlaIaIaTyGlyHisPheGlyArgAspAspAlaAs 378
    |||||||
210 CTTCACTCGCGAGGTGGTCAAGCCC 234
    |||||||
378 pPheThrTrpGluValValLysPro 386

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seq_name: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:AAW34541

seq_documentation_block:

ID AAW34541 standard; protein; 394 AA.

AC AAW34541;

XX 26-MAR-1998 (first entry)

XX S-adenosylmethionine synthase 2.

XX S-adenosylmethionine synthase 2; sam2; barley; alkali resistant plant.

OS Hordeum vulgare.

XX JP09313186-A.

XX 09-DEC-1997.

XX 28-MAY-1996; 96JP-0133406.

XX 28-MAY-1996; 96JP-0133406.

XX (NIOC) NIPPON OIL CO LTD.

DR WPI: 1998-080077/08.

DR N-PSDB; AAT99142.

PT S-adenosyl-methionine synthase gene - useful in producing plants resistant to alkaline soil

XX Claim 2; Page 6-7; 13pp; Japanese.

CC This sequence represents the S-adenosylmethionine synthase 2 (sam2) protein. The DNA encoding this sequence may be used in producing plants which are resistant to alkaline soil.

XX Sequence 394 AA;

alignment_scores:

Quality: 127.00 Length: 25
Ratio: 5.292 Gaps: 0
Percent Similarity: 96.000 Percent Identity: 96.000

alignment_block:

US-09-198-779B-1 x AAW34541 ..

Align seg 1/1 to: AAW34541 from: 1 to: 394

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160 AGGTTTCATCAAGACCGCGCATACGGCCACTTTGGCCGTGACGACGCCGA 209
    |||||||
362 ArgPheIleLysThrAlaIaIaTyGlyHisPheGlyArgAspAspAlaAs 378
    |||||||
210 CTTCACTCGCGAGGTGGTCAAGCCC 234
    |||||||
378 pPheThrTrpGluValValLysPro 386

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seq_name: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:AAW34542

seq_documentation_block:

ID AAW34542 standard; protein; 394 AA.

AC AAW34542;

XX 26-MAR-1998 (first entry)

XX S-adenosylmethionine synthase 3.

XX S-adenosylmethionine synthase 3; sam3; barley; alkali resistant plant.

OS Hordeum vulgare.

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PN JP09313186-A.
XX
XX 09-DEC-1997.
XX
XX 28-MAY-1996; 96JP-0133406.
XX
XX 28-MAY-1996; 96JP-0133406.
XX
XX (NIOC ) NIPPON OIL CO LTD.
XX
XX WPI; 1998-080077/08.
XX
XX N-PSDB; AAT99143.
XX
XX S-adenosyl-methionine synthase gene - useful in producing plants
XX resistant to alkaline soil
XX
XX
XX Claim 3; Page 7-8; 13pp; Japanese.
XX
XX This sequence represents the S-adenosylmethionine synthase 3 (sam3)
XX protein. The DNA encoding this sequence may be used in producing plants
XX which are resistant to alkaline soil.
XX
XX
SQ Sequence 394 AA:

alignment_scores:
    Quality: 127.00      Length: 25
    Ratio: 5.292        Gaps: 0
    Percent Similarity: 96.000      Percent Identity: 96.000

alignment_block:
    US-09-198-779B-1 x AAW34542 ..

Align seg 1/1 to: AAW34542 from: 1 to: 394

160 AGGTTTCATCAAGACCGCGCATACGGCCACTTTGGCCGTGACGACGCCGA 209
    |||||||
362 ArgPheIleLysThrAlaAlaIatyrGlyHisPheGlyArgAspAlaAs 378
210 CTTCACTGCGAGGTGTCAGGCC 234
    |||||||
378 PPherThrPrpGluValValLysPro 386

seq_name: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:AAW97744

seq_documentation_block:
ID AAW97744 standard; Protein; 394 AA.
XX
XX AAW97744;
XX
XX 21-MAY-1999 (first entry)
XX
XX wheat S-adenosylmethionine synthetase.
XX
XX S-Adenosylmethionine synthetase; wheat; amino acid; lysine;
XX threonine; methionine; cysteine; isoleucine; transgenic plant;
XX crop improvement; food; feedstuff.
XX
XX Triticum aestivum.
XX
XX
XX Key Location/Qualifiers
XX
XX FT Misc-difference 93 /note- "encoded by AAR"
XX
XX FT Misc-difference 150 /note- "encoded by CTY"
XX
XX FT Misc-difference 155 /note- "encoded by ACS"
XX
XX FT Misc-difference 282 /note- "encoded by CGY"
XX
XX FT Misc-difference 290 /note- "encoded by CAR"
XX
XX
XX W09855601-A2.

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XX
XX 10-DEC-1998.
XX
XX 05-JUN-1998; 98MO-US11692.
XX
XX 12-JUN-1997; 970S-0049443.
XX
XX 06-JUN-1997; 970S-0048771.
XX
XX (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
XX Abell LM, Allen SM, Falco SC, Hiltz WD, Kinney AJ;
XX Rafalski JA, Thorpe CJ;
XX
XX WPI; 1999-070263/06.
XX
XX N-PSDB; AAX07185.
XX
XX
XX Example 7; Page 70-71; 98pp; English.
XX
XX This is the amino acid sequence of a full-length wheat
XX S-adenosylmethionine synthetase, as deduced from a cDNA contig (see
XX AAX07185) obtained from kernel, leaf, seedling and root cDNA clones.
XX The wheat enzyme shows sequence similarity to the barley enzyme.
XX The invention relates to new isolated nucleic acid fragments (see
XX AAX07168-85) encoding plant enzymes (see AAW97727-44) that catalyse
XX steps in the biosynthesis of lysine, threonine, methionine,
XX cysteine and isoleucine from aspartate, the enzyme being selected
XX from dihydropicolinate reductase, diaminopimelate epimerase,
XX threonine synthase, threonine deaminase or S-adenosylmethionine
XX synthetase. The invention also relates to the construction of a
XX chimeric gene encoding all or a portion of the biosynthetic pathway
XX enzyme, in sense or antisense orientation, where expression of the
XX chimeric gene results in production of altered levels of the enzyme
XX in a transformed host cell. Overexpression or reduction of
XX expression of genes encoding the amino acid biosynthetic pathway
XX enzymes in crop plants such as corn, soybean and wheat can be used
XX to alter levels of the amino acids in human food and animal feed.
XX Transformed host cells can also be used to identify compounds that
XX inhibit one of the enzymes.
XX
XX
SQ Sequence 394 AA:

alignment_scores:
    Quality: 127.00      Length: 25
    Ratio: 5.292        Gaps: 0
    Percent Similarity: 96.000      Percent Identity: 96.000

alignment_block:
    US-09-198-779B-1 x AAW97744 ..

Align seg 1/1 to: AAW97744 from: 1 to: 394

160 AGGTTTCATCAAGACCGCGCATACGGCCACTTTGGCCGTGACGACGCCGA 209
    |||||||
362 ArgPheIleLysThrAlaAlaIatyrGlyHisPheGlyArgAspAlaAs 378
210 CTTCACTGCGAGGTGTCAGGCC 234
    |||||||
378 PPherThrPrpGluValValLysPro 386

seq_name: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:AAG34556

seq_documentation_block:
ID AAG34556 standard; Protein; 47 AA.
XX
XX AAG34556;
XX
XX 18-OCT-2000 (first entry)
XX

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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159684.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160747.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
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PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

alignment_scores:

Quality: 125.00 Length: 25
Ratio: 5.208 Gaps: 0
Percent Similarity: 96.000 Percent Identity: 92.000

alignment_block:

US-09-198-779B-1 x AAG34556

Align seg 1/1 to: AAG34556 from: 1 to: 47

160 AGGTTGATCAAGACCGCGCATACGGCCACTTTGGCCGTGACGACGCCGA 209
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15 ArpheleuysthrAlaIatYrGLHisphcGLyArGAspAraIaAs 31
210 CTTGACCTGGCAGGTGTTCAAGCCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
31 pPheThrTpGLyValIValIyLysPro 39

seq_name: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AAG2000.DAT:AAG07762

seq_documentation_block:

ID AAG07762 standard; Protein; 342 AA.
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AC AAG07762;
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana protein fragment SEQ ID NO: 5038.
XX
XX Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.
XX Arabidopsis thaliana.
OS
PN EP1033405-A2.
XX
XX 06-SEP-2000.
PD
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
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PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
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PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
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PR 17-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
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PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.

PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
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PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
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PR 04-OCT-1999; 99US-0157117.
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PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0158293.
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PR 22-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

alignment_scores:
Quality: 125.00 Length: 25
Ratio: 5.208 Gaps: 0
Percent Similarity: 96.000 Percent Identity: 92.000

alignment block:
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XX
DT 18-OCT-2000 (first entry)
XX
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XX
KW Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
XX
XX Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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Ratio: 5.208         Caps: 0
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XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX EP1033405-A2.
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XX 25-FEB-2000; 2000EP-0301439.
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18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 46640.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hydridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PE 25-FEB-2000; 2000EP-0301439.

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Align seg 1/1 to: AAG37872 from: 1 to: 344

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DT 18-OCT-2000 (first entry)
XX
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seq_documentation_block:

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DT 06-SEP-1999 (first entry)

DE S-adenosyl methionine (SAM) partial sequence.

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KW plant maturation; S-adenosyl methionine; flower; fruit development.

Phaseolus vulgaris.

PN W09929159-A1.

PD 17-JUN-1999.

PF 08-DEC-1998; 98WO-US25799.

PR 08-DEC-1997; 97US-0067898.

PA (VITA-) VITALITY BIOTECHNOLOGIES INC.

PI Gepstein S, Hajuote T, Rosner A;

WPI; 1999-404873/34.

DR N-PSDB; AAX81128

PT DNA encoding senescence-associated genes for a senescence

PT receptor-like protein kinase

PS Example 1; Fig 4; 70pp; English.

The invention relates to a senescence-associated receptor-like protein kinase (Sark) gene. The sark gene is a senescence-associated gene (sag) and is expressed early in the plant senescence process. The sark gene promoter is useful for driving expression of foreign genes having a desired product, such as a pharmaceutical, during the process of plant maturation. The sark gene promoter can be used to drive expression of resistance genes against pathogens or pests during senescence when the plant is particularly susceptible to infection or infestation. The sark gene promoter may also be used to drive expression of a gene encoding an inhibitor of senescence. Plant senescence may be inhibited by use of antisense sark constructs. Over expression of the sag genes, using the sark or sam (S-adenosyl methionine) gene promoters is useful for induction of early senescence. This is useful to obtain flower or fruit development prior to specific pest onset, prior to undesirable cross-fertilization from related crops, at a specific time during storage or retail, or to avoid development of plant structures that are not of agronomic importance. The present sequence represents a partial sequence of S-adenosyl methionine (SAM).

Sequence 64 AA;

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XX 17-OCT-2000 (first entry)
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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OS Arabidopsis thaliana.
XX
EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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DT 17-OCT-2000 (first entry)

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KM Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

XX Arabidopsis thaliana.

PN EP1033405-A2.

XX EP1033405-A2.

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XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

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DE
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KM crop improvement; food; feedstuff.
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PI Rafalski JA, Thorpe CJ;
PI
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XX WPI: 1999-070263/06.
DR N-FSDB; AAX07183.
DR
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PT encode: dihydrodipicolinate reductase; diaminopimelate epimerase;
PT threonine synthase; threonine deaminase; S-adenosylmethionine
PT synthetase
XX
XX Example 7; Page 63-64; 98pp: English.
PS
XX
XX This is the amino acid sequence of a full-length corn
CC S-adenosylmethionine synthetase, as deduced from a cDNA clone (see
CC AAX07183), designated cc3.m00002.d2, obtained from a corn callus
CC cDNA library. The corn enzyme shows sequence similarity to the
CC Oryza sativa enzyme. The invention relates to new isolated
CC nucleic acid fragments (see AAX07168-85) encoding plant enzymes (see

```

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CC AAW97727-44) that catalyse steps in the biosynthesis of lysine,
CC threonine, methionine, cysteine and isoleucine from aspartate, the
CC enzyme being selected from dihydrodipicolinate reductase,
CC diaminopimelate epimerase, threonine synthase, threonine deaminase
CC or S-adenosylmethionine synthetase. The invention also relates to
CC the construction of a chimeric gene encoding all or a portion of
CC the biosynthetic pathway enzyme, in sense or antisense orientation,
CC where expression of the chimeric gene results in production of
CC altered levels of the enzyme in a transformed host cell.
CC Overexpression or reduction of expression of genes encoding the
CC amino acid biosynthetic pathway enzymes in crop plants such as
CC corn, soybean and wheat can be used to alter levels of the amino
CC acids in human food and animal feed. Transformed host cells can
CC also be used to identify compounds that inhibit one of the enzymes.
XX
SQ Sequence 396 AA;

alignment_scores:
    Quality: 117.00      Length: 25
    Ratio: 5.087        Gaps: 0
    Percent Similarity: 92.000    Percent Identity: 84.000

alignment_block:
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364 ArgTyrLeuLysThrAlaIaTyrGlyHisPheGlyArgGluAspProAs 380
210 CTTGACCTGCGAGGTGTCAGGCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
380 pPheTrpGluValIaLysPro 388

seq_name: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA1999.DAT:AAW97743

seq_documentation_block:
ID AAW97743 standard; Protein: 392 AA.
AC AAW97743;
XX
DT 21-MAY-1999 (first entry)
XX
DE Soybean S-adenosylmethionine synthetase.
XX
KW S-Adenosylmethionine synthetase; soybean; amino acid; lysine;
KW threonine; methionine; cysteine; isoleucine; transgenic plant;
KW crop improvement; food; feedstuff.
XX
OS Glycine max.
XX
PN WO9855601-A2.
XX
PD 10-DEC-1998.
XX
PF 05-JUN-1998; 98WO-US11692.
XX
PR 12-JUN-1997; 97US-0049443.
XX
PR 06-JUN-1997; 97US-0048771.
XX
PA (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI Abell LM, Allen SM, Falco SC, Hiltz WD, Kinney AJ;
PI Rafalski JA, Thorpe CJ;
XX
DR WPI: 1999-070263/06.
DR N-PSDB: AAX07184.
XX
PT New plant amino acid biosynthetic enzymes, DNA and chimeric genes -
PT encode: dihydrodipicolinate reductase; diaminopimelate epimerase;
PT threonine synthase; threonine deaminase; S-adenosylmethionine
```

```
PT synthetase
XX
XX Example 7; Page 67-68; 98pp; English.
XX
CC This is the amino acid sequence of a full-length soybean
CC S-adenosylmethionine synthetase, as deduced from a cDNA clone (see
CC AAX07184), designated s2.12b06, obtained from a soybean seed
CC cDNA library. The soybean enzyme shows sequence similarity to the
CC tomato enzyme. The invention relates to new isolated nucleic acid
CC fragments (see AAX07168-85) encoding plant enzymes (see AAW97727-44)
CC that catalyse steps in the biosynthesis of lysine, threonine,
CC methionine, cysteine and isoleucine from aspartate, the enzyme
CC being selected from dihydrodipicolinate reductase,
CC diaminopimelate epimerase, threonine synthase, threonine deaminase
CC or S-adenosylmethionine synthetase. The invention also relates to
CC the construction of a chimeric gene encoding all or a portion of
CC the biosynthetic pathway enzyme, in sense or antisense orientation,
CC where expression of the chimeric gene results in production of
CC altered levels of the enzyme in a transformed host cell.
CC Overexpression or reduction of expression of genes encoding the
CC amino acid biosynthetic pathway enzymes in crop plants such as
CC corn, soybean and wheat can be used to alter levels of the amino
CC acids in human food and animal feed. Transformed host cells can
CC also be used to identify compounds that inhibit one of the enzymes.
XX
SQ Sequence 392 AA;

alignment_scores:
    Quality: 116.00      Length: 25
    Ratio: 5.043        Gaps: 0
    Percent Similarity: 92.000    Percent Identity: 84.000

alignment_block:
US-09-198-779b-1 x AAW97743 ..

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seq_name: /SIBS1/gcdata/geneseq/geneseqp-emb1/AA2000.DAT:AA606945

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AC AA606945;
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XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 3909.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
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PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
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PR 29-MAR-1999; 990S-0126785.
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alignment_scores:
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279 ArgPheGlnLysThrAlaIaIaTyGlyHisPheGlyArgAspAspProAs 295
210 CTTCACTCGGAGTGTGTCAAGCCC 234
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295 PheThrTrpGluValValLysPro 303

seq_name: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:AAG39109

seq_documentation_block:

ID AAG39109 standard; Protein: 341 AA.

XX AAG39109;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 48343.

XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

PD 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

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XX KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
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XX OS Arabidopsis thaliana.
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XX PN EP1033405-A2.
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Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

OS Arabidopsis thaliana.

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Ratio: 5.227 Gaps: 0
Percent Similarity: 88.000 Percent Identity: 88.000

alignment_block:
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332 AcgPhgGlnLysThrAlaIatYgLnIsPhgGlyAraGAspAspTrpAs 348
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ID AAG06943 standard; Protein; 368 AA.

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XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 3907.

XX Protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS EP1033405-A2.
XX
XX PD 06-SEP-2000.
XX
XX PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
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PR 04-MAY-1999; 99US-0132487.
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Quality: 5.227 Gaps: 0
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alignment_block:
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Align seg 1/1 to: AAG06943 from: 1 to: 368

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210 CTTACCTCGCAGGAGTGTCAGACCC 234
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352 pPheThrTrpGluValValysPro 360

seq_name: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT: AAG39108

seq_documentation_block:
ID AAG39108 standard; Protein; 390 AA.

XX AAG39108;

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XX DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 48342.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP103405-A2.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
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PR 06-APR-1999; 99US-0128234.
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Ratio: 5.227 Gaps: 0
Percent Similarity: 88.000 Percent Identity: 88.000

alignment_block:

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210 CTTACACGTGCGAGGTGTCACGCC 234
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377 pPheThrTrpGluValIValLysPro 385

seq_name: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT: AAG40366

seq_documentation_block:

ID AAG40366 standard; Protein: 393 AA.

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XX 18-OCT-2000 (first entry)
DT Arabidopsis thaliana protein fragment SEQ ID NO: 50077.
XX
DE Protein identification: signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 9905-0121825.
PR 05-MAR-1999; 9905-0123180.
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Percent Similarity: 88.000 Percent Identity: 88.000

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361 ATGPhcgluylsthrAlaIatrygrLyspHeGLyArGAspAspProAs 377
210 CTTCACCTCGAGAGTGCTCAAGCCC 234
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377 pPhetHrtrpGluValIValIysPro 385

seq_name: /SIDS1/gcdata/geneseq/geneseq-emb1/AA2000.DAT: AAG39107
seq_documentation_block:

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AC
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XX 18-OCT-2000 (first entry)
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XX Arabidopsis thaliana protein fragment SEQ ID NO: 48341.
DE
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XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
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XX
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  Ratio: 5.227        Gaps: 0
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410 ArgpHeGlnLysThrAlaIatYrgLHsPheGlyArgAspAspProAs 426
210 CTTCACTCGAGAGGTGGTCAAGCCC 234
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426 pPheThrTrpGluValValLysPro 434

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  28-MAR-2001 (first entry)

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  Nicotiana tabacum S-adenosylmethionine synthetase (SAMS).

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  Tobacco; alkaloid; nicotine; transgenic plant; pharmaceutical protein;
  herbicide resistance; S-adenosylmethionine synthetase; SAMS.

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  Nicotiana tabacum.

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  WO200067558-A1.

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  16-NOV-2000.

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  05-MAY-2000; 2000WO-US12450.

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  06-MAY-1999; 99US-0132919.

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  (TIMK/) TIMKO M.

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  Timko M;

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  WPI: 2001-007279/01.

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  N-PSDB; AAD02296.

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```

  New nucleic acid encoding alkaloid-synthesis enzymes in tobacco, useful
  e.g. for producing transgenic plants with altered nicotine content.

```

```

  Claim 17; Page 79-81; 103pp; English.

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```

  The invention relates to enzymes involved in alkaloid, specifically
  nicotine, synthesis in tobacco and nucleic acids encoding them. The
  CC nucleic acid of the invention can be used, in sense or antisense
  CC orientation, to produce transgenic tobacco plants with altered
  CC alkaloid content, and also for expression of exogenous proteins,
  CC e.g. pharmaceutical proteins or proteins implicated in resistance
  CC to herbicides. The protein of the invention can be used to
  CC identify modulators of enzymatic activity in plants.
  CC The present sequence is Nicotiana tabacum S-adenosylmethionine
  CC synthetase (SAMS). This enzyme is involved in the nicotine
  CC biosynthetic pathway.

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  S0 Sequence 390 AA;

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Align seg 1/1 to: AAV72078 from: 1 to: 390

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377 pPheSerTrpGluThrValLys 384

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seq_name: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:AAI18652
seq_documentation_block:
  ID AAI18652 standard: Protein; 332 AA.

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XX AC AAB18652;
XX XX
XX DT 22-JAN-2001 (first entry)
XX DE
XX XX Amino acid sequence of an ORF15 partial S-adenosylmethionine synthase.
XX KM Nardoniolide synthase; polyketide synthase gene; nardoniolide polyketide;
XX KM antibiotic; C12-hydroxylase; pick; desosamine biosynthesis;
XX KM desosaminyl transferase enzyme; ketolide; beta-glucosidase enzyme;
XX KM plicromycin biosynthesis; S-adenosylmethionine synthase.
XX OS
XX PN Streptomyces venezuelae.
XX XX
XX PD US6117659-A.
XX PD 12-SEP-2000.
XX PF 27-MAY-1999; 99US-0320878.
XX PF
XX PR 28-MAY-1998; 98US-0087080.
XX PR 22-SEP-1998; 98US-0100880.
XX PR 08-FEB-1999; 99US-0119139.
XX PR 20-MAY-1999; 99US-0134990.
XX PR 30-APR-1997; 97US-0846247.
XX PR 06-MAY-1998; 98US-0073538.
XX PR 28-AUG-1998; 98US-0141908.
XX PA
XX PI (KOSA-) KOSAN BIOSCIENCES INC.
XX PI Ashley G, Betlach MC, Betlach M, Tang L, McDaniel R;
XX DR WPI: 2000-610844/58.
XX XX
XX PT New recombinant pick hydroxylase gene of Streptomyces venezuelae useful
XX PT for converting ketolides to antibiotics and as antibiotics and
XX PT intermediates in the synthesis of compounds with pharmaceutical value
XX PS
XX PS Disclosure; Columns 39-40; 117pp; English.
XX XX
XX CC The present sequence represents a partial S-adenosylmethionine synthase.
XX CC The nucleotide sequence encoding it is used in the course of the
XX CC invention. The specification describes a recombinant DNA compound
XX CC expressing recombinant polyketide synthase genes in host cells for the
XX CC production of nardoniolide, nardoniolide derivatives and polyketides that
XX CC are useful as antibiotics and as intermediates in the synthesis of
XX CC compounds with pharmaceutical value. The DNA compounds may also encode
XX CC a C12-hydroxylase (pick), desosamine biosynthesis and desosaminyl
XX CC transferase enzymes (useful for conversion of ketolides to antibiotics),
XX CC and the beta-glucosidase enzyme (involved in plicromycin biosynthesis).
XX CC These compounds are also useful for increasing the antibiotic activity
XX CC of a compound relative to the unhydroxylated compound. The recombinant
XX CC host cells are useful as genetic systems that allow rapid engineering
XX CC of the nardoniolide polyketide synthase. These would be valuable for
XX CC creating novel ketolide analogs for pharmaceutical applications.
XX XX
XX SQ Sequence 332 AA;

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  Ratio: 4.375      Gaps: 0
Percent Similarity: 80.000      Percent Identity: 65.000

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Align seg 1/1 to: AAB18652 from: 1 to: 332

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315 eThrTrpGln 318

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AC AA67216;
XX XX
XX DT 23-MAR-2000 (first entry)
XX XX
XX DE ORF 15 encoded S-adenosylmethionine synthase (SAM synthase).
XX KM Nardoniolide polyketide synthase; PKS; desosamine biosynthesis; ketolide;
XX KM SAM synthase; S-adenosylmethionine synthase; antibiotic production;
XX KM nardomycin; plicromycin.
XX XX
XX OS Streptomyces venezuelae.
XX PN
XX PD WO961599-A2.
XX PF
XX PD 02-DEC-1999.
XX PF
XX PR 27-MAY-1999; 99WO-US11814.
XX PR
XX PR 28-MAY-1998; 98US-0087080.
XX PR 28-AUG-1998; 98US-0141908.
XX PR 22-SEP-1998; 98US-0100880.
XX PR 08-FEB-1999; 99US-0119139.
XX XX
XX PA (KOSA-) KOSAN BIOSCIENCES INC.
XX PI
XX PI Ashley G, Betlach MC, Betlach M, McDaniel R, Tang L;
XX DR WPI: 2000-072618/06.
XX DR N-PSDB; AA256005.
XX XX
XX PT New recombinant DNA encoding a domain of nardoniolide polyketide
XX PT synthase, for production of ketolide antibiotics -
XX PS
XX PS Example 2; Page 33-34; 98pp; English.
XX XX
XX CC This is the Streptomyces venezuelae S-adenosylmethionine synthase, SAM
XX CC synthase amino acid sequence, encoded by ORF15. This protein is involved
XX CC in desosamine biosynthesis. The invention relates to recombinant DNA
XX CC containing a coding sequence for a nardoniolide polyketide synthase
XX CC (PKS). Polyketides are compounds synthesised from 2-carbon units through
XX CC a series of condensations and subsequent modifications. Modular PKSs are
XX CC responsible for the production of many antibiotics including plicromycin.
XX CC The nardoniolide PKS consists of a loading module, six extender modules,
XX CC and two thioester domains. Four proteins make up the nardoniolide PKS
XX CC (PICAI, PICAIR, PICAIRI and PICAIIV). PICAI includes the loading module
XX CC and extender modules 1 and 2, PICAIRI includes extender modules 3 and 4,
XX CC PICAIRII includes extender module 5 and PICAIIV includes extender module 6
XX CC and a type II thioesterase domain. The second type II thioesterase
XX CC domain is found on the PICB protein. The nucleotide sequences encoding
XX CC all of these proteins can be isolated in recombinant form from the
XX CC recombinant cosmid PKOS023-27 (see AA256001). Nardoniolide is
XX CC desosaminylated in S. venezuelae to yield nardomycin, the desosaminyl
XX CC transferase enzyme is required for this conversion, and the desosamine
XX CC biosynthetic genes are also found in cosmid PKOS023-27. The recombinant
XX CC DNA of the invention is used to express, in transformed cells,
XX CC nardoniolide (or its derivatives) or other ketolides (particularly
XX CC hybrids), which may then be converted (e.g. by other enzymes
XX CC recombinantly expressed in the same hosts) to polyketide antibiotics or
XX CC their intermediates. The antibiotics are useful in human or veterinary
XX CC medicine.
XX XX
XX SQ Sequence 332 AA;

```

alignment_scores: Ratio: 70.00 Length: 20
Percent Similarity: 80.000 Gaps: 0
alignment_block:
US-09-198-779b-1 x AAV67216 ..
Align seg 1/1 to: AAV67216 from: 1 to: 332
163 TTCATCAAGACCGCCGATACGGCCACTTTGGCCGTGACGACGCCGACTT 212
 ::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
299 TYSERGLNTHRALAALATYRGLYHISPHGGLYARGGLULNEUPROASPH 315
213 CACCTGCGAG 222
 ||||| |||||
315 ETHRRTPGLU 318
seq_name: /SIDSI/gcdata/geneseq/geneseqp-emb1/AA1994.DAT:AA54204
seq_documentation_block:
ID AAR54204 standard; Protein: 402 AA.
XX
AC AAR54204;
XX
DT 18-NOV-1994 (first entry)
XX
DE snac gene product involved in streptogramin biosynthetic pathway.
XX
KW Antibiotic; streptogramin; snac; snab; snac; biosynthesis; enzyme;
KW biosynthetic pathway; Streptomyces pristinaespiralis.
XX
OS Streptomyces pristinaespiralis.
XX
PN FR696189-A.
XX
PD 01-APR-1994.
XX
PF 25-SEP-1992; 92FR-0011441.
XX
PR 25-SEP-1992; 92FR-0011441.
XX
PA (RHON) RHONE POULENC RORER SA.
XX
PI Blanc V, Blanche F, Crouzet J, Jacques N, Lacroix P;
PI Ribaut D, Zagorec M;
XX
DR WPI: 1994-128286/16.
DR N-PSDB; AAG64204.
XX
XX DNA involved in streptogramin antibiotic biosynthesis - for
PT prodn. or bio-conversion of streptogramin(s) or prodn. of
PT streptogramin intermediates, derivs. or hybrid antibiotics
XX
PS Claim 21, Page 55-57; 83pp; French.
XX
XX The snac gene product is involved in the biosynthesis of
CC streptogramins, antibiotics active against Gram positive bacteria.
CC The identification of the sequences encoding the enzymes involved
CC in the biosynthetic pathway means that they can be isolated and
CC manipulated. Mutant microorganisms in which a step in the
CC streptogramin biosynthetic pathway is blocked can be cultured to
CC produce streptogramin intermediates, which may later be converted
CC to streptogramin derivatives. Recombinant cells may also be used
CC for the bioconversion of streptogramins from one form to another or
CC for the production of hybrid antibiotics.
XX
SQ Sequence 402 AA;

alignment_scores: Quality: 69.00 Length: 20

Ratio: 4.600 Gaps: 0
Percent Similarity: 75.000 Percent Identity: 65.000
alignment_block:
US-09-198-779b-1 x AAR54204 ..
Align seg 1/1 to: AAR54204 from: 1 to: 402
163 TTCATCAAGACCGCCGATACGGCCACTTTGGCCGTGACGACGCCGACTT 212
 ::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
369 TYRALAALATHRALAALATYRGLYHISPHGGLYARGGLULNEUPROASPH 385
213 CACCTGCGAG 222
 ||||| |||||
385 ETHRRTPGLU 388
seq_name: /SIDSI/gcdata/geneseq/geneseqp-emb1/AA2001.DAT:AAU71922
seq_documentation_block:
ID AAU71922 standard; Protein: 407 AA.
XX
AC AAU71922;
XX
DT 26-FEB-2002 (first entry)
XX
DE C. glutamicum metabolic pathway protein encoded by gene #57.
XX
KW Metabolic pathway protein; MP; lysine biosynthesis pathway;
KW methionine biosynthesis pathway; large-scale production of fine chemical;
KW Corynebacterium diptheriae; diptheria.
XX
OS Corynebacterium glutamicum.
XX
PN WO200166573-A2.
XX
PD 13-SEP-2001.
XX
PF 22-DEC-2000; 2000WO-IB02035.
XX
PR 09-MAR-2000; 2000US-187970P.
PR 23-JUN-2000; 2000US-0606740.
XX
PA (BADI) BASF AG.
XX
PI Pompejus M, Kroeger B, Schroeder H, Zelder O, Haberhauer G, Kim J;
PI Lee H, Hwang B;
XX
DR WPI: 2001-582269/65.
DR N-PSDB; AAS96132.
XX
XX Nucleic acids encoding metabolic pathway proteins from Corynebacterium
PT glutamicum, useful for producing methionine and lysine in
PT Corynebacterium and Brevibacterium -
XX
PS Disclosure; Page 311-312; 316pp; English.
XX
XX The present invention relates to the isolation of novel Corynebacterium
CC glutamicum genes (AAS96073-AAS96132) encoding metabolic pathway (MP)
CC proteins. The metabolic pathway proteins of the invention
CC include enzymes involved in the lysine and methionine biosynthetic
CC pathways. The polynucleotide sequences of the invention can be used
CC for the large-scale production and/or modulation of expression of
CC fine chemicals such as lysine and methionine. The sequences of the
CC invention may be used to identify C. glutamicum and related organisms
CC e.g. C. diptheriae in a subject to detect diptheria.
CC AAU71863-AAU71922 represent the novel C. glutamicum metabolic pathway
CC proteins of the invention.
XX
SQ Sequence 407 AA;

alignment_scores: Quality: 67.00 Length: 22

Ratio: 4.188 Gaps: 0
Percent Similarity: 72.727 Percent Identity: 54.545
Alignment_block:
US-09-198-779B-1 x AAU71922 ..

Align seg 1/1 to: AAU71922 from: 1 to: 407

163 TTCATCAAGACGGCGCATACGCGCACTTGGCGGTGACGACGCGACTT 212
::: ||||||||||||||||||||| ||| |||:
373 TyralaaSprThrAlaAlaIatYrGlyHisphgIyArGrThrAspLeuAspLe 389
213 CACCTCGCAGGTGTC 228
: |||:::
389 uProtRpGluaIaile 394

seq_name: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:AA691519

seq_documentation_block:

ID AAG91519 standard; Protein; 407 AA.

XX AAG91519;

DT 26-SEP-2001 (first entry)

DE C glutamicum protein fragment SEQ ID NO: 5273.

KW Corynebacterium; amino acid synthesis; vitamin; saccharide;

KM organic acid synthesis.

XX Corynebacterium glutamicum.

PN EP1108790-A2.

PD 20-JUN-2001.

PF 18-DEC-2000; 2000EP-0127688.

PR 16-DEC-1999; 99JP-0377484.

PR 07-APR-2000; 2000JP-0159162.

PR 03-AUG-2000; 2000JP-0280988.

XX (KYOW) KYOWA HAKKO KOGYO KK.

PI Nakagawa S, Mizoguchi H, Ando S, Hayashi M, Ochiai K, Yokoi H;

PI Tateishi N, Senoh A, Ikeda M, Ozaki A;

DR WPI; 2001-376931/40.

DR N-PSDB; AAH66738.

XX Novel polynucleotides derived from Corynebacterium bacteria, for identifying

PT mutation point of a gene, measuring expression of a gene, analysing

PT expression profile or pattern of a gene and identifying homologous gene

PT -

XX Claim 17; SEQ ID NO: 5273; 246pp + Sequence Listing; English.

XX The present invention provides a number of nucleotide and protein

CC sequences from the Corynebacterium glutamicum. These

CC are useful for identifying the mutation point of a gene derived from a

CC mutant of corynebacterium, measuring expression amount and

CC analysing the expression profile or expression pattern of a gene derived

CC from Corynebacterium, and identifying a homolog of a gene derived

CC from corynebacterium. Corynebacterium bacteria are useful for producing

CC amino acids, nucleic acids, vitamins, saccharides and organic acids,

CC particularly L-lysine. The present sequence is a protein described

CC in the exemplification of the invention.

CC Note: The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from the

CC European Patent Office.

XX Sequence 407 AA;

SO

alignment_scores: Quality: 67.00 Length: 22
Ratio: 4.188 Gaps: 0
Percent Similarity: 72.727 Percent Identity: 54.545
Alignment_block:
US-09-198-779B-1 x AAG91519 ..

Align seg 1/1 to: AAG91519 from: 1 to: 407

163 TTCATCAAGACGGCGCATACGCGCACTTGGCGGTGACGACGCGACTT 212
::: ||||||||||||||||||||| ||| |||:
373 TyralaaSprThrAlaAlaIatYrGlyHisphgIyArGrThrAspLeuAspLe 389
213 CACCTCGCAGGTGTC 228
: |||:::
389 uProtRpGluaIaile 394

seq_name: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:AAB79754

seq_documentation_block:

ID AAB79754 standard; Protein; 407 AA.

XX AAB79754;

DT 30-APR-2001 (first entry)

DE Corynebacterium glutamicum MP protein sequence SEQ ID NO:242.

KW Corynebacterium glutamicum; metabolic pathway protein; MP protein;

KM fine chemical production; microorganism; organic acid; nucleoside;

KW nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide;

KM lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;

KW carbohydrate; aromatic compound; cofactor; polypeptide; enzyme.

XX Corynebacterium glutamicum.

PN WO200100843-A2.

PD 04-JAN-2001.

PF 23-JUN-2000; 2000WO-IB00923.

PR 25-JUN-1999; 99US-0141031.

PR 01-JUL-1999; 99DE-1030476.

PR 02-JUL-1999; 99US-0142101.

PR 08-JUL-1999; 99DE-1031415.

PR 08-JUL-1999; 99DE-1031418.

PR 08-JUL-1999; 99DE-1031419.

PR 08-JUL-1999; 99DE-1031420.

PR 08-JUL-1999; 99DE-1031424.

PR 08-JUL-1999; 99DE-1031428.

PR 08-JUL-1999; 99DE-1031434.

PR 08-JUL-1999; 99DE-1031435.

PR 08-JUL-1999; 99DE-1031443.

PR 08-JUL-1999; 99DE-1031453.

PR 08-JUL-1999; 99DE-1031457.

PR 08-JUL-1999; 99DE-1031465.

PR 08-JUL-1999; 99DE-1031478.

PR 08-JUL-1999; 99DE-1031510.

PR 08-JUL-1999; 99DE-1031541.

PR 08-JUL-1999; 99DE-1031573.

PR 08-JUL-1999; 99DE-1031592.

PR 08-JUL-1999; 99DE-1031632.

PR 08-JUL-1999; 99DE-1031634.

PR 08-JUL-1999; 99DE-1031636.

PR 08-JUL-1999; 99DE-1032125.

PR 08-JUL-1999; 99DE-1032126.

PR 08-JUL-1999; 99DE-1032130.

PR 08-JUL-1999; 99DE-1032186.

PR 08-JUL-1999; 99DE-1032206.

PR 08-JUL-1999; 99DE-1032227.

```

163 TTTATCAAGACGCCCCATCAGCGGCACATTGGGCGGTGACGACGCGGACTT 212
   ::: ||||| |::| |::| |::| |::| |::| |::| |::| |::| |::|
373 TyrrhalasphthralalalaIyrlYhisPhegIyatrgrmrAspleubmsple 389msple
      : |||::: |::: |::: |::: |::: |::: |::: |::: |::: |:::
213 CACCCTGGAGAGTGTC 228

```

immunosuppressive: extra-intestinal infection: rhvlgenev: morbillivir:
 km escherichia coli; B2/D+A-; antinflammatory; antibacterial;
 KW

KM systemic infection; non-diarrhoeal infection; septicaemia;
KM pyelonephritis; antibiotic resistance.
XX
OS Escherichia coli.
XX
PN WO200166572-A2.
XX
PD 13-SEP-2001.
XX
PF 12-MAR-2001; 2001WO-EP03445.
XX
PR 10-MAR-2000; 2000FR-0003145.
PR 02-FEB-2001; 2001FR-0001449.
XX
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PI Bingen E, Bonacorsi S, Clermont O, Nassif X, Tinsley C;
PI WPI; 2001-550253/61.
XX
DR A library of DNA fragments of Escherichia coli strains for the
XX phylogenetic determination of a given strain comprises polynucleotides of
PT nature B2/D+ A -
PT Example 6; Fig 6; 646pp; English.
XX
PS The invention relates to a library of DNA fragments of Escherichia coli
CC strains comprising polynucleotides (ABA88577-ABA88729 and ABA89533)
CC and encoded proteins (ABBS2459-ABBS2919 and ABBS2934-ABBS3094) of nature
CC B2/D+A-. The polynucleotides have potential anti-inflammatory,
CC antibacterial and immunosuppressive activity as part of pharmaceutical
CC compositions used to treat, palliate or prevent extra-intestinal E. coli
CC infections. The polypeptides are useful for determining the phylogenic
CC group of a given E. coli strain. These polypeptides can detect and treat
CC an undesired development of E. coli, particularly an extra-intestinal
CC infection that include systemic and non-diarrhoeal infections such as
CC septicaemia, pyelonephritis and meningitis this is particularly
CC advantageous as bacterial resistance is increasing with the more
CC frequent use of broad spectrum antibiotics.
XX
SQ Sequence 383 AA;

alignment_scores:
Quality: 64.00 Length: 22
Ratio: 3.765 Gaps: 1
Percent Similarity: 77.273 Percent Identity: 63.636

alignment_block:
US-09-198-779B-1 x ABBS2815 ..

Align seg 1/1 to: ABBS2815 from: 1 to: 383

160 AGGTCATCAAGACCGCGCATACGGCCACTTGGCCGTGACGACGCCGA 209
||||: |||||||:|||||||:|||||||:|||||||:|
351 ArgylrtrglgyltrhrAlaCystyrGlyHisphelgArGaSp.....Se 365
210 CTTCACCTGCGCAGGTG 225
:|||| |||||
365 rPhEPrOTrPGLuVal 370

seq_name: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:AAU33382

seq_documentation_block:
ID AAU33382 standard; Protein; 386 AA.
XX
AC AAU33382;
XX
DT 14-FEB-2002 (first entry)
XX
DE Enterococcus faecalis cellular proliferation protein #18.
XX
KW Antisense; prokaryotic cellular proliferation protein;

KM antibiotic; antibacterial; drug design.
XX
OS Enterococcus faecalis.
XX
PN WO200170955-A2.
XX
PD 27-SEP-2001.
XX
PF 21-MAR-2001; 2001WO-US09180.
XX
PR 21-MAR-2000; 2000US-191078P.
PR 23-MAY-2000; 2000US-206848P.
PR 26-MAY-2000; 2000US-207272P.
PR 23-OCT-2000; 2000US-242578P.
PR 27-NOV-2000; 2000US-253625P.
PR 22-DEC-2000; 2000US-257931P.
PR 16-FEB-2001; 2001US-269308P.
XX
PA (ELITR-) ELITRA PHARM INC.
PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
PI N-PSDB; AAS51241.
DR WPI; 2001-611495/70.
DR N-PSDB; AAS51241.
XX
PT New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -
XX
XX Example 3; Seq ID No 4878; 511pp; English.

The invention relates to antisense inhibitors of genes essential to
prokaryotic cellular proliferation, their use in identifying the
genes, their use in the discovery of novel antibiotics, the essential
genes themselves and the encoded proteins. The prokaryotes used are
Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
invention is also useful for the identification of potential new targets
for antibiotic development. The antisense nucleic acids can also be used
to identify proteins used in proliferation, to express these proteins,
and to obtain antibodies capable of binding to the expressed proteins.
The proteins can be used to screen compounds in rational drug discovery
programmes. The antisense nucleic acid sequence is also useful to screen
for homologous nucleic acids which are required for cell proliferation in
a wide variety of organisms. The present sequence represents an
essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 386 AA;

alignment_scores:
Quality: 64.00 Length: 18
Ratio: 4.571 Gaps: 0
Percent Similarity: 77.778 Percent Identity: 66.667

alignment_block:
US-09-198-779B-1 x AAU33382 ..

Align seg 1/1 to: AAU33382 from: 1 to: 386

169 AAGACCGCGCATACGGCCACTTGGCCGTGACGACGCCGACTTCACCTG 218
:::|||||||:|||||||:|||||||:|||||||:|||||||:|
360 GlnthrAlaAlaIatyrGlyHisphelgYArgtrhrAspIeaSpIeuPrOTr 376
219 CGAG 222
|||
376 pGlu 377

seq_name: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:AAU35173

seq_documentation_block:

ID AUA35173 standard; Protein; 394 AA.

XX AUA35173;

DT 13-FEB-2002 (first entry)

DE Enterococcus faecalis cellular proliferation protein #460.

KW Antisense; prokaryotic cellular proliferation protein;
antibiotic; antibacterial; drug design.

XX Enterococcus faecalis.

XX WO200170955-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US09180.

XX 21-MAR-2000; 2000US-191078P.

XX 23-MAY-2000; 2000US-206848P.

XX 26-MAY-2000; 2000US-207727P.

XX 23-OCT-2000; 2000US-242578P.

XX 27-NOV-2000; 2000US-253625P.

XX 22-DEC-2000; 2000US-257931P.

XX 16-FEB-2001; 2001US-269308P.

XX (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;

XX WPI: 2001-611495/70.

XX N-PSDB; AAS53032.

XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids -

XX Example 3; Seq ID No 10766; 51pp; English.

XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the
CC genes, their use in the discovery of novel antibiotics, the essential
CC genes themselves and the encoded proteins. The prokaryotes used are
CC Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella
CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The
CC invention is also useful for the identification of potential new targets
CC for antibiotic development. The antisense nucleic acids can also be used
CC to identify proteins used in proliferation, to express these proteins,
CC and to obtain antibodies capable of binding to the expressed proteins.
CC The proteins can be used to screen compounds in rational drug discovery
CC programmes. The antisense nucleic acid sequence is also useful to screen
CC for homologous nucleic acids which are required for cell proliferation in
CC a wide variety of organisms. The present sequence represents an
CC essential prokaryotic cellular proliferation protein.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 394 AA;

alignment_scores:

Quality: 64.00 Length: 18
Ratio: 4.571 Gaps: 0
Percent Similarity: 77.778 Percent Identity: 66.667

alignment_block:

US-09-198-779b-1 x AUA35173 ..

Align seg 1/1 to: AUA35173 from: 1 to: 394

169 AAGACGCCGCATACGGCAGCTTTGGCCGTGACAGCGCAGCTTCACCTG 218

363 GlnThrAlaIatYrGlyHisPheGlyArgThrAspIleAspLeuProTr 379

219 CGAG 222

379 pGlu 380

seq_name: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AUA2001.DAT.ABG25556

seq_documentation_block:

ID ABG25556 standard; Protein; 94 AA.

XX ABG25556;

XX 18-FEB-2002 (first entry)

XX Novel human diagnostic protein #25547.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI: 2001-639362/73.

XX N-PSDB; AAS89743.

XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity

XX Claim 20; SEQ ID No 55915; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 94 AA;

alignment_scores: Quality: 63.00 Length: 55
 Ratio: 2.100 Gaps: 1
Percent Similarity: 54.545 Percent Identity: 32.727

alignment_block:
US-09-198-779B-1/rev x ABG25556 ..

Align seg 1/1 to: ABG25556 from: 1 to: 94

226 CCACCTCCGACGAGTGAAGTCGGCGGTGCATGACGGCCAAAGTGGCGGTATGCG 177
 ||| ||| ||||| ||| ||| ||||| |||
12 ProAlaArgProGlnSerArgLeuAlaHisArgGlnArgGlyArgMetAr 28

176 GCGGCTTGATGACCTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 127
 | ||| ::: ||| ::: ||| :::
28 g.GlyAlaProArgProPheArgGlnArgGlnIleLysLeuCySTyrAla 44

126 NNNNNAAGTACGTGTGTGTCCTGTCATATATACACATTATATACAC 77
 ||| ::: ||| ||| ||| ||| ||| ||| |||
45 ArgCysThrProThrIleCysProThrIlySerArgSerArSnth 61

76 AAGCAACATGGA 64
 |::: ::: |||
61 rValThrSerGly 65

seq_name: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:ABG22853

seq_documentation_block:
ID ABG22853 standard; Protein: 398 AA.
XX
AC ABG22853:
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #22844.
XX
KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR N-PSDB: AAS87040.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity
PS Claim 20: SEQ ID No 53212; 103pp: English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.

SO Sequence 398 AA;

alignment_scores: Quality: 63.00 Length: 21
 Ratio: 3.938 Gaps: 1
Percent Similarity: 76.190 Percent Identity: 66.667

alignment_block:
US-09-198-779B-1 x ABG22853 ..

Align seg 1/1 to: ABG22853 from: 1 to: 398

169 AAGACCGCCGATACGCGCCACTTTGGCGGTGACGACGCCGACTTCACCTG 218
 ::: ||||| ||||| ||||| ||||| ||||| ||| |||
376 ArgTrnAlaAlaIlyrGlyHisPheGlyArgAsp.....SerPheProTr 390

219 CGAGGTGTCAG 231
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390 pGluValProLys 394

seq_name: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA1997.DAT:AAW20562

seq_documentation_block:
ID AAW20562 standard; Protein: 104 AA.
XX
AC AAW20562:
XX
DT 17-JUL-1997 (first entry)
XX
DE H. pylori cytoplasmic protein 677088.aa.
XX
KW Cytoplasmic; vaccine; prevention; treatment; infection; identification;
KW binding compound; bacterium; life cycle; activator; bacteria; inhibitor;
KW duodenal ulcer disease; chronic gastritis; diagnosis; envelope.
XX
OS Helicobacter pylori.
XX
PN WO9640893-A1.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US09122.
XX
PR 01-APR-1996; 96US-0630405.
PR 07-JUN-1995; 95US-0487032.
XX
PA (ASTR) ASTRA AB.
XX
PI Berglindh OT, Smith D, Mellgaard BL;
XX
DR WPI: 1997-052306/05.
DR N-PSDB: AAT67709.
XX
XX Helicobacter pylori nucleic acid sequences and related
PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori
PT infection, and to detect Helicobacter


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XX 06-JUN-1996; 96WO-US09122.
PF
XX
PR 01-APR-1996; 96US-0630405.
PR 07-JUN-1995; 95US-0487032.
XX
PA (ASTR ) ASTRA AB.
XX
PI Berglinde OT, Smith D, Mellgaard BL;
XX
DR WPI; 1997-052306/05.
DR N-PSDB; AAT68254.
XX
PT Helicobacter pylori nucleic acid sequences and related
PT polypeptide(s) - useful for vaccines to treat or prevent H. pylori
PT infection, and to detect Helicobacter
XX
XX
PS Claim 61; Page 1392; 1481pp; English.
XX
CC The present sequence is a H. pylori cytoplasmic protein involved in
CC nucleotide metabolism.
CC The protein may be used in a vaccine to prevent or treat H. pylori
CC infection or to identify H. pylori polypeptide binding compounds,
CC useful as potential H. pylori life cycle activators or inhibitors.
CC The genomic sequence of H. pylori (ATCC 55679) was determined from
CC overlapping contigs generated by mechanically shearing the bacterial
CC DNA. The sequences were analysed for ORF of at least 180 nucleotides,
CC and the predicted coding regions defined by computer evaluation. To
CC identify likely H. pylori antigens for vaccine development, the amino
CC acid sequences predicted from various ORF were analysed for significant
CC homology to other known or exported membrane proteins. Having identified
CC and determined the sequences of interest, particular regions can be
CC isolated from H. pylori by PCR amplification for recombinant polypeptide
CC production, e.g. in E. coli hosts.
XX
SQ Sequence 253 AA;

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alignment_scores:
  Quality: 61.00      Length: 17
  Ratio: 4.357      Gaps: 0
  Percent Similarity: 82.353      Percent Identity: 64.706

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alignment_block:
US-09-198-779B-1 x AAW21001 ..

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Align seg 1/1 to: AAW21001 from: 1 to: 253

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172 ACCGCGCATACGCGCACTTGGCGTGACGACGCGGACTTCACCTGCCA 221
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223 ThrSerAlaIyrGlyHisPheGlyArgGluLeuGluGluPheThrTrpG1 239

222 G 222
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239 u 239

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APPLICANT: BETLACH, Mary C.
APPLICANT: MCDANIEL, Robert
APPLICANT: TANG, Li
TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
FILE REFERENCE: 300622002120
CURRENT FILING DATE: 1999-05-27
EARLIER FILING DATE: 1999-05-27
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-08-28
EARLIER FILING DATE: 1998-05-06
EARLIER FILING DATE: 1997-04-30
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1998-09-22
EARLIER FILING DATE: 1998-09-22
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 332
TYPE: PRT
ORGANISM: Streptomyces venezuelae
US-09-320-878-16

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Quality: 70.00 Length: 20
Ratio: 4.375 Gaps: 0
Percent Similarity: 80.000 Percent Identity: 65.000

alignment_block:

US-09-198-779b-1 x US-09-320-878-16 ..

Align seg 1/1 to: US-09-320-878-16 from: 1 to: 332

163 TTCATCAGACCGCGCATACGCGCACTTTGGCCGTGACGACCGCCGACTT 212
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299 TTTTGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 315
213 CACCTCGCAG 222
||| |||
315 eThrTrpGlu 318

seq_name: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:US-08-403-852D-19

seq_documentation_block:

Sequence 19, Application US/08403852D
Patent No. 5891695
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
TITLE OF INVENTION: Polypeptides Involved In The
Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/403,852D
FILING DATE: 10-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806,0054-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
STRANDNESS: single
TOPOLOGY: linear
US-08-403-852D-19

alignment_scores:
Quality: 69.00 Length: 20
Ratio: 4.600 Gaps: 0
Percent Similarity: 75.000 Percent Identity: 65.000

alignment_block:

US-09-198-779b-1 x US-08-403-852D-19 ..

Align seg 1/1 to: US-08-403-852D-19 from: 1 to: 402

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369 TTTTGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 385
213 CACCTCGCAG 222
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385 eThrTrpGlu 388

seq_name: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:US-08-510-646B-20

seq_documentation_block:

Sequence 20, Application US/08510646B
Patent No. 6077699
GENERAL INFORMATION:
APPLICANT: Blanc, Veronique
APPLICANT: Blanche, Francis
APPLICANT: Crouzet, Joel
APPLICANT: Jacques, Nathalie
APPLICANT: Lacroix, Patricia
APPLICANT: Thibaut, Denis
APPLICANT: Zagorec, Monique
APPLICANT: Debussche, Laurent
TITLE OF INVENTION: Polypeptides Involved In The
Biosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & Dunner

COUNTRY: USA

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1 STREET: 1300 I Street, N.W., Suite 700
2 City: Washington
3 STATE: D.C.
4 COUNTRY: USA
5 ZIP: 20005-3315
6 COMPUTER READABLE FORM:
7 MEDIUM TYPE: Floppy disk
8 COMPUTER: IBM PC compatible
9 OPERATING SYSTEM: PC-DOS/MS-DOS
10 SOFTWARE: Patent Release #1.0, Version #1.30
11 CURRENT APPLICATION DATA:
12 APPLICATION NUMBER: US/09/231,818
13 FILING DATE:
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: US/08/403,852
16 FILING DATE: 10-MAY-1995
17 APPLICATION NUMBER: PCT/FR 93/00923
18 FILING DATE: 25-SEP-1993
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: FR 92/11441
21 FILING DATE: 25-SEP-1992
22 ATTORNEY/AGENT INFORMATION:
23 NAME: Meyers, Kenneth J.
24 REGISTRATION NUMBER: 25,146
25 REFERENCE/DOCKET NUMBER: 03806.0054-00000
26 TELECOMMUNICATION INFORMATION:
27 TELEPHONE: (202) 408-4000
28 TELEFAX: (202) 408-4400
29 INFORMATION FOR SEQ ID NO: 19:
30 SEQUENCE CHARACTERISTICS:
31 LENGTH: 402 amino acids
32 TYPE: amino acid
33 STRANDEDNESS: single
34 TOPOLOGY: linear
35 US-09-231-818-19
36
37 alignment scores:
38 Quality: 69.00 Length: 20
39 Ratio: 4.600 Gaps: 0
40 Percent Similarity: 75.000 Percent Identity: 65.000
41
42 alignment block:
43 US-09-198-779B-1 x US-09-231-818-19 ..
44
45 Align seg 1/1 to: US-09-231-818-19 from: 1 to: 402
46
47 163 TTGATCATGAGCCGCGCATACGCGCATTGGCGTGACGAGCGCCACTT 212
48 :: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
49 369 TYRALAALAThRALAALATyrGLYhISPhnEGLYATgLGILeuPRoAsPh 385
50 213 CACCTGCGAG 222
51 |||| |||
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54 seq_name: /cgn2_6/ptodata/2/1aa/5A_COWB pep:US-08-339-152A-21
55
56 seq_documentation_block:
57 ; Sequence 21, Application US/08339152A
58 ; Patent No. 5643726
59 ; GENERAL INFORMATION:
60 ; APPLICANT: Tanzi, Rudolph E.
61 ; APPLICANT: Kovacs, Dora M.
62 ; TITLE OF INVENTION: Methods For Modulating Transcription
63 ; TITLE OF INVENTION: From The Anyloid -Protein Precursor (APP) Promote
64 ; NUMBER OF SEQUENCES: 33
65 ; CORRESPONDENCE ADDRESSES:
66 ; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
67 ; STREET: 1100 New York Ave., NW, Suite 600
68 ; CITY: Washington
69 ; STATE: DC
70 ; COUNTRY: USA
71 ; ZIP: 20005
72

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,152A
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 0609,4120000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
TELEX:
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-339-152A-21

alignment_scores:
Quality: 55.50      Length: 19
Ratio: 3.469        Gaps: 1
Percent Similarity: 84.211  Percent Identity: 63.158

alignment_block:
US-09-198-779b-1/rev x US-08-339-152A-21  ..
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22 ThrAlaGlnValGlnAlaIaIaSerSer...ProArgTrpProGlnIleAl 37

174 GGTCTTG 168
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37 aValIeu 39

seq_name: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:US-08-007-999B-12
seq_documentation_block:
Sequence 12, Application US/08007999B
Patent No 5851787
GENERAL INFORMATION:
APPLICANT: Masco, Wilma
APPLICANT: Bupp, Keith
APPLICANT: Magendantz, Margaret
APPLICANT: Tanzi, Rudolph
APPLICANT: Solomon, Frank
TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES
NUMBER OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESS: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
STREET: 1100 New York Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/007,999B
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/872,642
FILING DATE: 20-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,022
FILING DATE: 17-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: 0609,3520002/JAG/GKT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)371-2571
TELEFAX: (202)371-2540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-007-999B-12

alignment_scores:
Quality: 55.50      Length: 19
Ratio: 3.469        Gaps: 1
Percent Similarity: 84.211  Percent Identity: 63.158

alignment_block:
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22 ThrAlaGlnValGlnAlaIaIaSerSer...ProArgTrpProGlnIleAl 37

174 GGTCTTG 168
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37 aValIeu 39

seq_name: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:US-08-689-276A-12
seq_documentation_block:
Sequence 12, Application US/08689276A
Patent No 5891991
GENERAL INFORMATION:
APPLICANT: Masco, Wilma
APPLICANT: Bupp, Keith
APPLICANT: Magendantz, Margaret
APPLICANT: Tanzi, Rudolph
APPLICANT: Solomon, Frank
TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES
NUMBER OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESSES:
ADDRESS: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/689,276A
FILING DATE: 06-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/007,999
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,642
FILING DATE: 20-APR-1992
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PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/930,022
 FILING DATE: 17-AUG-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: JORGE A. GOLDSTEIN
 REGISTRATION NUMBER: 29,021
 REFERENCE/DOCKET NUMBER: 0609.3520003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)371-2571
 TELEFAX: (202)371-2540
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 197 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-689-276A-12

[illegible]

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alignmentblock:
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22 Thrtaadlnvalnlmnlmnlmnlmnlmnlmnlmnlmnlmnlmnlmnlmnlmnl 37
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
174 GGTCTTG 168
|||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
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seq_name: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:US-09-273-686-2

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seq documentation block:
: Sequence 2, Application US/09273686
: Patent No. 6228625
:
: GENERAL INFORMATION:
:
: APPLICANT: Zalacain, Magdalena
: APPLICANT: Burnham, Martin K. R.
: APPLICANT: Biswas, Sanjoy
: APPLICANT: Brown, James
: APPLICANT: Ingraham, Karen, A.
: APPLICANT: Chalker, Alison F.
: APPLICANT: So, Chi Y.
: APPLICANT: Holmes, David J.
: APPLICANT: Van Horn, Stephanie
: APPLICANT: Warren, Richard L.
: TITLE OF INVENTION: metk
: FILE REFERENCE: GM0176
: CURRENT APPLICATION NUMBER: US/09/273,686
: CURRENT FILING DATE: 1999-03-22
: EARLIER APPLICATION NUMBER: 60/106,767
: EARLIER FILING DATE: 1998-11-03
: NUMBER OF SEQ ID NOS: 3
: SOFTWARE: FastSeq for Windows Version 3.0.
:
: SEQ ID NO 2
:
: LENGTH: 396
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: TYPE: PRT
:
: ORGANISM: Streptococcus pneumoniae
:
: US-09-273-686-2

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alignment_scores:		
Quality:	55.00	Length: 18
Ratio:	3.929	Gaps: 0
Percent Similarity:	77.778	Percent Identity: 55.556

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alignment_block:
US-09-198-779B-1 x US-09-273-686-2      ..
Align seg 1/1  to: US-09-273-686-2  from: 1  to: 396

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169 AAGACGCCGCATATAGCGACCTTTGGCGCTGACGACGCCGACTTCACCTG 218
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seq_name: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:US-08-333-901-1

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seq.documentation_block:
  Sequence 1, Application US/08333901
  Patent No. 5599906
  GENERAL INFORMATION:
    APPLICANT: Dasamhapatra, Bimalendu
    TITLE OF INVENTION: No. 5599906el Protease Assays
    NUMBER OF SEQUENCES: 5
    CORRESPONDENCE ADDRESS:
      ADDRESSEE: Schering-Plough Corporation
      STREET: One Giralda Farms
      CITY: Madison
      STATE: New Jersey
      COUNTRY: USA
      ZIP: 07940
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: Apple Macintosh
    OPERATING SYSTEM: Macintosh 6.0.5
    SOFTWARE: Microsoft Word 5.1a
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/08/333,901
    FILING DATE: 03-NOV-1994
    CLASSIFICATION: 435
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 07/923,988
    FILING DATE: 21-SEP-1992
    APPLICATION NUMBER: PCT/US91/02283
    FILING DATE: 10-APR-1991
    APPLICATION NUMBER: 07/509,007
    FILING DATE: 13-APR-1990
    ATTORNEY/AGENT INFORMATION:
      NAME: Dulak, No. 5599906man C.
  INFORMATION FOR SEQ ID NO: 1:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 881 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
  MOLECULE TYPE: peptide
  US-08-333-901-1

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  quality: 55.00
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270 GlnIleuLeuIleAlaSerLysAspGlnTrpGlnIleuPheAsnGlySII 286
74 GTTGCTGTTAATAATGTTGTAATTAATGACGACACACANCA 113
||||| : ||||| : ||||| : ||||| : ||||| :
286 eleuAlaIleGluValAsnProGlySIIeuleuLysIleuThr 299

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seq_name: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:US-08-456-582-1
seq_documentation_block:
; Sequence 1, Application US/08456582
; Patent No. 5721133
; GENERAL INFORMATION:
; APPLICANT: Dasmahapatra, Bimalendu
; TITLE OF INVENTION: No. 5721133el Protease Assays
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Schering-Plough Corporation
; STREET: One Giralda Farms
; CITY: Madison
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07940
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,582
; FILING DATE: 01-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/923,988
; FILING DATE: 21-SEP-1992
; APPLICATION NUMBER: PCT/US91/02283
; FILING DATE: 10-APR-1991
; APPLICATION NUMBER: 07/509,007
; FILING DATE: 13-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Dulak, No. 5721133man C.
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 881 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-456-582-1

alignment_scores:
Quality: 55.00 Length: 30
Ratio: 2.750 Gaps: 0
Percent Similarity: 66.667 Percent Identity: 36.667

alignment_block:
US-09-198-779B-1 x US-08-456-582-1 ..
Align seg 1/1 to: US-08-456-582-1 from: 1 to: 881

24 CAGATGACGCTGCCATGCTGATAAATGACGCGTCTGATCCATGTC 73
|||||: ||| |||: ||| |||: ||| |||: ||| |||: |||
270 GlnIleGlnIleAlaSerLysAspGlnTrpGlnIleLeuPheAsnCysI1 286
74 GTTGTTATTAATGTTGTAATATGACGACGACACACA 113
|||||: ||| |||: ||| |||: ||| |||: ||| |||: |||
286 eleuAlaIleGlyAlaTrpCysIleGluGlyGluSerThr 299

seq_name: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:US-08-898-789-1
seq_documentation_block:
; Sequence 1, Application US/08898789
; Patent No. 5891635
; GENERAL INFORMATION:
; APPLICANT: Dasmahapatra, Bimalendu
; TITLE OF INVENTION: No. 5891635el Protease Assays
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESS: Schering-Plough Corporation
```

```
STREET: One Giralda Farms
CITY: Madison
STATE: New Jersey
COUNTRY: USA
ZIP: 07940
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/898,789
FILING DATE: 23-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/923,988
FILING DATE: 21-SEP-1992
APPLICATION NUMBER: PCT/US91/02283
FILING DATE: 10-APR-1991
APPLICATION NUMBER: 07/509,007
FILING DATE: 13-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Dulak, No. 5891635man C.
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 881 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-898-789-1

alignment_scores:
Quality: 55.00 Length: 30
Ratio: 2.750 Gaps: 0
Percent Similarity: 66.667 Percent Identity: 36.667

alignment_block:
US-09-198-779B-1 x US-08-898-789-1 ..
Align seg 1/1 to: US-08-898-789-1 from: 1 to: 881

24 CAGATGACGCTGCCATGCTGATAAATGACGCGTCTGATCCATGTC 73
|||||: ||| |||: ||| |||: ||| |||: ||| |||: |||
270 GlnIleGlnIleAlaSerLysAspGlnTrpGlnIleLeuPheAsnCysI1 286
74 GTTGTTATTAATGTTGTAATATGACGACGACACACA 113
|||||: ||| |||: ||| |||: ||| |||: ||| |||: |||
286 eleuAlaIleGlyAlaTrpCysIleGluGlyGluSerThr 299

seq_name: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:US-09-039-555B-16
seq_documentation_block:
; Sequence 16, Application US/09039555B
; Patent No. 6033856
; GENERAL INFORMATION:
; APPLICANT: Koerner, Kathrin
; APPLICANT: Mueller, Rolf
; APPLICANT: Sadlaczek, Hans-Harald
; TITLE OF INVENTION: PROMOTER OF THE CDC25B GENE, ITS
; TITLE OF INVENTION: PREPARATION AND USE
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESS: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 07-OCT-1996

REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B96-010

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-571-758-2

alignment_scores:

Quality:	53.00	Length:	39
Ratio:	2.304	Gaps:	1
Percent Similarity:	58.974	Percent Identity:	35.897

alignment_block:

US-09-198-779B-1/rev x US-08-571-758-2 ..

Align seg 1/1 to: US-08-571-758-2 from: 1 to: 966

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121 AACGTACGTGTGTCCTGCTCAATTATACACATTAATAACACACGA 72
||| |||::: :: ::::: |||
87 AsngluArgIleProAlaAsngIyLeuValProHisThrInGlyAsngI 103
71 A.....CAATGATCAGACCGTCCATTATCAGCATGGCAGCGTCGA 28
| |||||::: ||| |||||
103 uLeuArgIInTrpLeuArgValIaGlyLeuSerGInGlyThrLeuThra 120
27 TCTGTCACGACGAGCTA 11
||| |||||
120 IacCysLeuAlaArgLeu 125
```

Fax: 515-294-2299
Email: schnable@iastate.edu
Primer A: TATACCATCACTTAAGCCG
Primer B: GAGACTTCGACTTCAGCC
PCR Profile:

Denaturation: 94 degrees C for 30 seconds
Annealing: 60 degrees C for 45 seconds
Polymerization: 72 degrees C for 90 seconds
PCR cycles: 31
Thermal cycler: Perkin Elmer TC
Protocol:

Template: 10-20 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Tag Polymerase: 0.05 units/uL
Total vol: 20 uL

Buffer:

MgCl2: 2 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.4.

FEATURES
source

Location/Qualifiers
1..305
/organism="Zea mays"
/strain="DE811"
/db_xref="taxon:4577"
/clone_id="maize leaf DNA"
/note="PCR products amplified from genomic DNA"
<1..>305

STS
BASE COUNT
ORIGIN
67 a 92 c 78 g 68 t

Query Match
Best Local Similarity 30.0%; Score 70.6; DB 11; Length 305;
Matches 73; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 159 caggttctcaagaccgcgcataagccacttggccgtgacgagccgacacttaactg 218
|||||
DB 276 CAGGTTCAATCAAGACCGCGGCTACGGCCTGACGCGTGACGACGCCGACTTACCTG 217

QY 219 cgaagtgtcaagcccc 235
|||||
DB 216 GGAGTGCTGAAGCCCC 200

RESULT 2
G71468/c 319 bp DNA linear STS 08-JUN-2001
LOCUS
DEFINITION A6003234FM017 maize leaf DNA Zea mays STS genomic, sequence tagged
site.

ACCESSION G71468
VERSION G71468.1 GI:14333153
KEYWORDS STS.
SOURCE Zea mays.
ORGANISM Zea mays.

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
JOURNAL 1 (bases 1 to 319)
Yang, Y.J., Guo, L., Ashlock, D.A., Wen, T.J. and Schnable, P.S.
3' UTR sequences of maize genes
Unpublished

COMMENT

Contact: Schnable, P.S.
Schnable Laboratory
Iowa State University
GA05 Agronomy Hall, Ames, IA 50011, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
Primer A: TATACCATCACTTAAGCCG

Primer B: GAGACTTCGACTTCAGCC
PCR Profile:

Denaturation: 94 degrees C for 30 seconds
Annealing: 60 degrees C for 45 seconds
Polymerization: 72 degrees C for 90 seconds
PCR cycles: 31
Thermal cycler: Perkin Elmer TC
Protocol:

Template: 10-20 ng
Primer: each 0.5 uM
dNTPs: each 200 uM
Tag Polymerase: 0.05 units/uL
Total vol: 20 uL

Buffer:

MgCl2: 2 mM
KCl: 50 mM
Tris-HCl: 20 mM
pH: 8.4.

FEATURES
source

Location/Qualifiers
1..319
/organism="Zea mays"
/strain="DE811"
/db_xref="taxon:4577"
/clone_id="maize leaf DNA"
/note="PCR products amplified from genomic DNA"
<1..>319

STS
BASE COUNT
ORIGIN
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Query Match
Best Local Similarity 29.4%; Score 69; DB 11; Length 319;
Matches 72; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 159 caggttctcaagaccgcgcataagccacttggccgtgacgagccgacacttaactg 218
|||||
DB 282 CAGGTTCAATCAAGACCGCGGCTACGGCCTTACGCGTGACGACGCCGACTTACCTG 223

QY 219 cgaagtgtcaagcccc 235
|||||
DB 222 GGAGTGCTGAAGCCCC 206

RESULT 3
E14404 1182 bp DNA linear PAT 28-JUL-1999
LOCUS
DEFINITION cDNA encoding S-adenosylmethionine synthetase.
ACCESSION E14404
VERSION E14404.1 GI:5709087
KEYWORDS JP 1997313186-A/3.
SOURCE Hordeum vulgare.
ORGANISM Hordeum vulgare.

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
JOURNAL Poolidae; Triticeae; Hordeum.
Mori, S.
1 (bases 1 to 1182)
GENE OF S-ADENOSYLMETHIONINE SYNTHASE
Patent: JP 1997313186-A 3 09-DEC-1997;
NIPPON OIL CO LTD
OS Hordeum vulgare
PN JP 1997313186-A/3
PD 09-DEC-1997
PE 28-MAY-1996 JP 1996133406
PI MORI SATOSHI
PC C12N15/09,C07H21/04,C12N9/00//A01H1/00,A01H5/00; CC
Strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH key
FH Location/Qualifiers

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 23:17:31 ; Search time 1925.22 Seconds
(without alignments)
2554.376 Million cell updates/sec

Title: US-09-198-779B-1

Perfect score: 235

Sequence: 1 gtttcgcgtctagctcgtt.....ctgcgagtgctcaagcccc 235

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hcg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_pn: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vi: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htg_inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match Length	ID	Description
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Result No.	Query	Score	Match Length	ID	Description
1	G70767/c	70.6	30.0	305 11	G70767
2	69	29.4	319	11	G71468
3	61.6	26.2	1182	6	E14404
4	61	26.0	1182	6	E14402
5	61	26.0	1353	8	BLXSNS
6	59.4	25.3	1182	6	E14403
7	56.2	23.9	1566	6	AF420238
8	56.2	23.9	1736	8	OSU82833
9	56.2	23.9	15064	2	AP003211
10	54.6	23.2	545	8	AY039010
11	54.6	23.2	1272	8	ACU17241
12	54.6	23.2	1437	8	POPSMDPT
13	51.6	22.0	1628	8	MCU79767
14	51.4	21.9	1547	8	AF004317
15	51.4	21.9	1659	8	AB062358
16	51.2	21.8	1632	8	DINCARAA
17	51	21.7	1594	8	OSA296743
18	51	21.7	2183	8	OSSAMS1
19	51	21.7	150954	2	AC087552
20	50.4	21.4	1107	8	AY061895
21	50.4	21.4	1440	8	AF428440
22	50.4	21.4	1459	8	AY052311
23	50.4	21.4	1508	8	AF325061
24	50.4	21.4	1510	8	AY037214
25	50.4	21.4	80167	8	AB022216
26	50.4	21.4	121668	8	AC022521
27	49.8	21.2	1539	8	AF170798
28	49.8	21.2	1665	8	AF367310
29	49.8	21.2	114950	8	AC006922
30	48.8	20.8	772	8	AF443869
31	48.8	20.8	1479	8	LESALMSGA
32	48.8	20.8	1534	8	CRSAMS1
33	48.8	20.8	2559	8	ATSHSAM
34	48.8	20.8	2559	8	ATSHSAM
35	48.2	20.5	1173	8	AF183891
36	48.2	20.5	1327	8	PEABENSTNA
37	48.2	20.5	1446	8	PSSAMS1
38	48.2	20.5	1455	8	LESALMSGC
39	48.2	20.5	1531	8	AF321001
40	48.2	20.5	1565	8	PHSAML
41	48.2	20.5	1627	8	AF346306
42	48	20.4	585	8	PUMMSA2A
43	47.2	20.1	4459	8	AF271220
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45	46.6	19.8	1572	8	AF346305

ALIGNMENTS

RESULT 1
LOCUS G70767/c
DEFINITION A60033234FB73 maize leaf DNA Zea mays STS genomic, sequence tagged site.
ACCESSION G70767
VERSION G70767.1 GI:14332452
KEYWORDS STS.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 305)
AUTHORS Yang,Y.T., Guo,L., Ashlock,D.A., Wen,T.J. and Schnable,P.S.
TITLE 3' UTR sequences of maize genes
JOURNAL Unpublished
COMMENT

Contact: Schnable, P.S.
Schnable Laboratory
Iowa State University
G405 Agronomy Hall, Ames, IA 50011, USA
Tel: 515-294-0975

US-09-791-537-120897

alignment_scores:

Quality: 118.00 Length: 25
Ratio: 5.130 Gaps: 0
Percent Similarity: 92.000 Percent Identity: 88.000

alignment_block:

US-09-198-779B-1 x US-09-791-537-120897 ..

Align seg 1/1 to: US-09-791-537-120897 from: 1 to: 394

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160 AGGTTTCATCAAGACCGCCGATACGGCCACTTTGGCCGTGACGAGCCGA 209
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362 ArgPheIleIySThrAlaIaIatrgIyHisPheGlyArgGluAspProAs 378
210 CTTCACTGCGAGGTGTCAAGCCC 234
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378 pPheThrTrpGluValValysPro 386

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seq_name: /cgn2_6/prodata/2/paa/US09_NEW_COMB.pep:US-10-155-881-25460

seq_documentation_block:

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; Sequence 25460, Application US/10155881
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jingdong
; APPLICANT: Lotliya, Linda L.
; APPLICANT: McIninch, James
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(15300)J
; CURRENT APPLICATION NUMBER: US/10/155,881
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 37595
; SEQ ID NO 25460
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-155-881-25460

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alignment_scores:

Quality: 118.00 Length: 25
Ratio: 5.130 Gaps: 0
Percent Similarity: 92.000 Percent Identity: 88.000

alignment_block:

US-09-198-779B-1 x US-10-155-881-25460 ..

Align seg 1/1 to: US-10-155-881-25460 from: 1 to: 436

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210 CTTCACTGCGAGGTGTCAAGCCC 234
|||||
420 pPheThrTrpGluValValysPro 428

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seq_name: /cgn2_6/prodata/2/paa/US09_NEW_COMB.pep:US-09-791-537-111090

seq_documentation_block:

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; Sequence 111090, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210

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; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 111090

; LENGTH: 393

; TYPE: PRT

; ORGANISM: Musa acuminata

US-09-791-537-111090

alignment_scores:

Quality: 117.00 Length: 25
Ratio: 5.087 Gaps: 0
Percent Similarity: 92.000 Percent Identity: 84.000

alignment_block:

US-09-198-779B-1 x US-09-791-537-111090 ..

Align seg 1/1 to: US-09-791-537-111090 from: 1 to: 393

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210 CTTCACTGCGAGGTGTCAAGCCC 234
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377 pPheThrTrpGluValValysPro 385

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361 ArgPheLeuLysThrAlaAlaIatYrGlyHisPheGlyArgAspAspProAs 377
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seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-791-537-120900

seq_documentation_block:

; Sequence 120900, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomimix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 120900
; LENGTH: 393
; TYPE: PRT
; ORGANISM: Catharanthus roseus
US-09-791-537-120900

alignment_scores:
Quality: 120.00 Length: 25
Ratio: 5.217 Gaps: 0
Percent Similarity: 92.000 Percent Identity: 88.000

alignment_block:

US-09-198-779b-1 x US-09-791-537-120900 ..

Align seg 1/1 to: US-09-791-537-120900 from: 1 to: 393

160 AGGTCATCAAGACCGCGCATACGGCCACTTTGGCCGTGAGAGCGCCGA 209
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361 ArgPheLeuLysThrAlaAlaIatYrGlyHisPheGlyArgAspAspProAs 377
210 CTTCACTCGAGGTGTCAGGCC 234
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377 pPheHrTrpGIuValValysPro 385

seq_name: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:US-10-155-881-37535

seq_documentation_block:

; Sequence 37535, Application US/10155881
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(15300)J
; CURRENT APPLICATION NUMBER: US/10/155,881
; CURRENT FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 37595
; SEQ ID NO 37535
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Glycine max
US-10-155-881-37535

alignment_scores:
Quality: 120.00 Length: 25
Ratio: 5.217 Gaps: 0
Percent Similarity: 92.000 Percent Identity: 88.000

alignment_block:

US-09-198-779b-1 x US-10-155-881-37535 ..

Align seg 1/1 to: US-10-155-881-37535 from: 1 to: 394

160 AGGTCATCAAGACCGCGCATACGGCCACTTTGGCCGTGAGAGCGCCGA 209
|||||:|||||
362 ArgPheLeuLysThrAlaAlaIatYrGlyHisPheGlyArgAspAspProAs 378
210 CTTCACTCGAGGTGTCAGGCC 234
||||| |||||||
378 pPheHrTrpGIuValValysPro 386

seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-791-537-51046

seq_documentation_block:

; Sequence 51046, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomimix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 51046
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Populus deltoides
US-09-791-537-51046

alignment_scores:
Quality: 120.00 Length: 25
Ratio: 5.217 Gaps: 0
Percent Similarity: 92.000 Percent Identity: 88.000

alignment_block:

US-09-198-779b-1 x US-09-791-537-51046 ..

Align seg 1/1 to: US-09-791-537-51046 from: 1 to: 395

160 AGGTCATCAAGACCGCGCATACGGCCACTTTGGCCGTGAGAGCGCCGA 209
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362 ArgPheLeuLysThrAlaAlaIatYrGlyHisPheGlyArgAspAspProAs 378
210 CTTCACTCGAGGTGTCAGGCC 234
||||| |||||||
378 pPheHrTrpGIuValValysPro 386

seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-791-537-120897

seq_documentation_block:

; Sequence 120897, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Biomimix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 120897
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Oryza sativa

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; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
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; LENGTH: 393
; TYPE: PRF
; ORGANISM: Arabidopsis thaliana
US-09-791-537-6453
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alignment_scores:
  Quality: 120.00      Length: 25
  Ratio: 5.217         Gaps: 0
  Percent Similarity: 92.000      Percent Identity: 88.000
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alignment_block:
US-09-198-779B-1 x US-09-791-537-6453 ..
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Align seg 1/1 to: US-09-791-537-6453 from: 1 to: 393
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210 CTTACCTGCGAGGTGTCAGAGCC 234
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377 pPheHrTpGlVAlVallySPrO 385
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seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-791-537-51038
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seq_documentation_block:
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; Sequence 51038, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 51038
; LENGTH: 393
; TYPE: PRF
; ORGANISM: Brassica juncea
US-09-791-537-51038
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alignment_scores:
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  Ratio: 5.217         Gaps: 0
  Percent Similarity: 92.000      Percent Identity: 88.000
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alignment_block:
US-09-198-779B-1 x US-09-791-537-51038 ..
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Align seg 1/1 to: US-09-791-537-51038 from: 1 to: 393
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210 CTTACCTGCGAGGTGTCAGAGCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
377 pPheHrTpGlVAlVallySPrO 385
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seq_name: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:US-09-791-537-85949
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; Sequence 85949, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY M-
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85949
; LENGTH: 393
; TYPE: PRF
; ORGANISM: Lycopersicon esculentum
US-09-791-537-85949
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alignment_scores:
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  Ratio: 5.217         Gaps: 0
  Percent Similarity: 92.000      Percent Identity: 88.000
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alignment_block:
US-09-198-779B-1 x US-09-791-537-85949 ..
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Align seg 1/1 to: US-09-791-537-85949 from: 1 to: 393
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210 CTTACCTGCGAGGTGTCAGAGCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
377 pPheHrTpGlVAlVallySPrO 385
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; Sequence 85952, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY M-
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85952
; LENGTH: 393
; TYPE: PRF
; ORGANISM: Lycopersicon esculentum
US-09-791-537-85952
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  Ratio: 5.217         Gaps: 0
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APPLICANT: Danzer, Joseph

OM of: US-09-198-779b-1 to: Pending_Patents_AA_New:* out_format : pfs

Date: Aug 20, 2002 2:52 AM

About: Results were produced by the Gencore software, version 4.5,
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-OUTFMT=pfs -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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/cgn2_6/ptodata/2/paa/US09_NEW.COMB.pcp:US-09-791-537-85952		120.00	290.74	2.6e-08		120.00	5.292	96.000	96.000
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/cgn2_6/ptodata/2/paa/US09_NEW.COMB.pcp:US-09-791-537-85952		116.00	281.06	8.6e-08		116.00	5.292	96.000	96.000
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/cgn2_6/ptodata/2/paa/US09_NEW.COMB.pcp:US-60-360-039-3052 + 74.00 170.12 0.136
/cgn2_6/ptodata/2/paa/US09_NEW.COMB.pcp:US-60-360-039-19703 + 73.00 167.68 0.191
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Sequence 42: Application US/09424978B
GENERAL INFORMATION:
APPLICANT: Falco, Saverio Carl
APPLICANT: Allen, Stephen M.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Hiltz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Abell, Lynne N.
TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
FILE REFERENCE: BB-1087
CURRENT APPLICATION NUMBER: US/09/424,978B
PRIOR APPLICATION NUMBER: 1999-12-02
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.1
SEQ ID NO 42
LENGTH: 394
TYPE: PRT
ORGANISM: Triticum aestiva
US-09-424-978B-42

alignment_scores:
Quality: 127.00 Length: 25
Ratio: 5.292 Gaps: 0
Percent Similarity: 96.000 Percent Identity: 96.000

alignment_block:
US-09-198-779b-1 x US-09-424-978B-42 ..

Align seg 1/1 to: US-09-424-978B-42 from: 1 to: 394

160 AGGTCATCAAGACGCGCATATCGCCATTGGCCGAGACGCCGA 209
|||||
362 AGPHEIIEIYTHRLALATYRIYHSPHEGLIYAGSPALIAAS 378

210 CTTACCTGCGAGTGTCACGCC 234
|||||

378 pPethertrpguValValyspro 386

seq_name: /cgn2_6/ptodata/2/paa/US09_NEW.COMB.pcp:US-09-791-537-124286

seq_documentation_block:

Sequence 124286: Application US/09791537
GENERAL INFORMATION:
APPLICANT: Biomomix, Inc.
APPLICANT: Debe, Derek
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PatentIn version 3.0
SEQ ID NO 124286
LENGTH: 394
TYPE: PRT
ORGANISM: Hordeum vulgare
US-09-791-537-124286

|||||
286 pphethrtprgluValValyspro 294

seq_name: /cgn2_6/ptodata/2/paa/US097_COMB.pep:US-09-708-427-50982

seq_documentation_block:

Sequence 50982, Application US/09708427

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: THEREBY

FILE REFERENCE: 2750-1243P

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTWARE: PatentIn version 3.1

SEQ ID NO 50982

LENGTH: 339

TYPE: PRT

ORGANISM: Zea mays subsp. mays

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..339

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc_feature

LOCATION: 1..339

OTHER INFORMATION: Ceres Seq. ID 1925818

US-09-708-427-50982

Alignment_scores:

Quality: 127.00 Length: 25

Ratio: 5.292 Gaps: 0

Percent Similarity: 96.000 Percent Identity: 96.000

alignment_block:

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Align seg 1/1 to: US-09-708-427-50982 from: 1 to: 339

160 AGGTTTCATCAGACCGCGCATACGGCCACTTTGGCGGTGACGACGCCGA 209

|||||

309 ArgpheiIeIySThrAlaIatyrGIyHspheGIyArgAspAspAlaAs 325

210 CTTCACTCGCAGGTGTCAGCCC 234

|||||

325 pphethrtprgluValValyspro 333

seq_name: /cgn2_6/ptodata/2/paa/US097_COMB.pep:US-09-708-427-50981

seq_documentation_block:

Sequence 50981, Application US/09708427

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: THEREBY

FILE REFERENCE: 2750-1243P

CURRENT APPLICATION NUMBER: US/09/708,427

CURRENT FILING DATE: 2000-11-09

NUMBER OF SEQ ID NOS: 85364

SOFTWARE: PatentIn version 3.1

SEQ ID NO 50981

LENGTH: 341

TYPE: PRT

ORGANISM: Zea mays subsp. mays

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..341

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc_feature

LOCATION: 1..341

OTHER INFORMATION: Ceres Seq. ID 1925817

US-09-708-427-50981

alignment_scores: Quality: 127.00 Length: 25

Ratio: 5.292 Gaps: 0

Percent Similarity: 96.000 Percent Identity: 96.000

alignment_block:

US-09-198-779b-1 x US-09-708-427-50981 ..

Align seg 1/1 to: US-09-708-427-50981 from: 1 to: 341

160 AGGTTTCATCAGACCGCGCATACGGCCACTTTGGCGGTGACGACGCCGA 209

|||||

311 ArgpheiIeIySThrAlaIatyrGIyHspheGIyArgAspAspAlaAs 327

210 CTTCACTCGCAGGTGTCAGCCC 234

|||||

327 pphethrtprgluValValyspro 335

seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-324-109-17286

seq_documentation_block:

Sequence 17286, Application US/60324109

GENERAL INFORMATION:

APPLICANT: Cao, Yongwei

APPLICANT: Edgerton, Michael D

APPLICANT: Hinkle, Gregory J.

APPLICANT: Kovalic, David K.

APPLICANT: Liu, Jindong

APPLICANT: Stein, Joshua

TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT

FILE REFERENCE: 38-10(52726)B

CURRENT APPLICATION NUMBER: US/60/324,109

CURRENT FILING DATE: 2001-09-21

NUMBER OF SEQ ID NOS: 33196

SEQ ID NO 17286

LENGTH: 351

TYPE: PRT

ORGANISM: Zea mays

FEATURE:

US-60-324-109-17286

alignment_scores: Quality: 127.00 Length: 25

Ratio: 5.292 Gaps: 0

Percent Similarity: 96.000 Percent Identity: 96.000

alignment_block:

US-09-198-779b-1 x US-60-324-109-17286 ..

Align seg 1/1 to: US-60-324-109-17286 from: 1 to: 351

160 AGGTTTCATCAGACCGCGCATACGGCCACTTTGGCGGTGACGACGCCGA 209

|||||

319 ArgpheiIeIySThrAlaIatyrGIyHspheGIyArgAspAspAlaAs 335

210 CTTCACTCGCAGGTGTCAGCCC 234

|||||

335 pphethrtprgluValValyspro 343

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; OTHER INFORMATION: Clone ID: 700430776_FLI
US-60-312-544-5922

alignment_scores:
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  Ratio: 5.292         Gaps: 0
  Percent Similarity: 96.000      Percent Identity: 96.000

alignment_block:
US-09-198-779B-1 x US-60-312-544-5922  ..

Align seg 1/1 to: US-60-312-544-5922 from: 1 to: 143

160 AGGTTTCATCAAGACCGCCGATACGCGCATTGGCCGTGACAGCCGCA 209
|||||
111 ArgpHeIlleYstHrAlaIaIatYrgLYHIsPheGlyAArgAspAspAlaAs 127
|||||
210 CTTTCACCTGCGAGGTGTCAAGCCC 234
|||||
127 pPheHtrTrpGIuValIySPro 135

seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-324-109-25804

seq_documentation_block:
; Sequence 25804, Application US/60324109
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)B
; CURRENT APPLICATION NUMBER: US/60/324,109
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 33196
; SEQ ID NO 25804
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
US-60-324-109-25804

alignment_scores:
  Quality: 127.00      Length: 25
  Ratio: 5.292         Gaps: 0
  Percent Similarity: 96.000      Percent Identity: 96.000

alignment_block:
US-09-198-779B-1 x US-60-324-109-25804  ..

Align seg 1/1 to: US-60-324-109-25804 from: 1 to: 220

160 AGGTTTCATCAAGACCGCCGATACGCGCATTGGCCGTGACAGCCGCA 209
|||||
188 ArgpHeIlleYstHrAlaIaIatYrgLYHIsPheGlyAArgAspAspAlaAs 204
|||||
210 CTTTCACCTGCGAGGTGTCAAGCCC 234
|||||
204 pPheHtrTrpGIuValIySPro 212

seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-324-109-26344

seq_documentation_block:
; Sequence 26344, Application US/60324109
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
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; APPLICANT: Liu, Jindong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)B
; CURRENT APPLICATION NUMBER: US/60/324,109
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 33196
; SEQ ID NO 26344
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
US-60-324-109-26344

alignment_scores:
  Quality: 127.00      Length: 25
  Ratio: 5.292         Gaps: 0
  Percent Similarity: 96.000      Percent Identity: 96.000

alignment_block:
US-09-198-779B-1 x US-60-324-109-26344  ..

Align seg 1/1 to: US-60-324-109-26344 from: 1 to: 262

160 AGGTTTCATCAAGACCGCCGATACGCGCATTGGCCGTGACAGCCGCA 209
|||||
230 ArgpHeIlleYstHrAlaIaIatYrgLYHIsPheGlyAArgAspAspAlaAs 246
|||||
210 CTTTCACCTGCGAGGTGTCAAGCCC 234
|||||
246 pPheHtrTrpGIuValIySPro 254

seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-312-544-6239

seq_documentation_block:
; Sequence 6239, Application US/60312544
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)A
; CURRENT APPLICATION NUMBER: US/60/312,544
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 10730
; SEQ ID NO 6239
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
US-60-312-544-6239

alignment_scores:
  Quality: 127.00      Length: 25
  Ratio: 5.292         Gaps: 0
  Percent Similarity: 96.000      Percent Identity: 96.000

alignment_block:
US-09-198-779B-1 x US-60-312-544-6239  ..

Align seg 1/1 to: US-60-312-544-6239 from: 1 to: 302

160 AGGTTTCATCAAGACCGCCGATACGCGCATTGGCCGTGACAGCCGCA 209
|||||
270 ArgpHeIlleYstHrAlaIaIatYrgLYHIsPheGlyAArgAspAspAlaAs 286
|||||
210 CTTTCACCTGCGAGGTGTCAAGCCC 234
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seq_documentation_block:
; Sequence 28766, Application US/60324109
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)B
; CURRENT APPLICATION NUMBER: US/60/324,109
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 33196
; SEQ ID NO 28766
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
US-60-324-109-28766

alignment_scores:
Quality: 127.00      Length: 25
Ratio: 5.292        Gaps: 0
Percent Similarity: 96.000      Percent Identity: 96.000

alignment_block:
US-09-198-779B-1 x US-60-324-109-28766 ..

Align seg 1/1 to: US-60-324-109-28766 from: 1 to: 116

160 AGGTCATCATAGAGCCGCGCATATAGCGCACTTGGCCGTGAGACGCCGA 209
|||||
84 ArgpheiIeIyStHrAlaIaIaTyrlGlyHIsPheGlyArgAspAspAlaAs 100
210 CTTCACCTGCGAGGTGTCAGCCCC 234
|||||
100 pPheHrTrpGIuValIaIySpro 108

seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-324-109-26158

seq_documentation_block:
; Sequence 26158, Application US/60324109
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)B
; CURRENT APPLICATION NUMBER: US/60/324,109
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 33196
; SEQ ID NO 26158
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
US-60-324-109-26158

alignment_scores:
Quality: 127.00      Length: 25
Ratio: 5.292        Gaps: 0
Percent Similarity: 96.000      Percent Identity: 96.000

alignment_block:
US-09-198-779B-1 x US-60-324-109-26158 ..

Align seg 1/1 to: US-60-324-109-26158 from: 1 to: 132

160 AGGTCATCATAGAGCCGCGCATATAGCGCACTTGGCCGTGAGACGCCGA 209
|||||
106 ArgpheiIeIyStHrAlaIaIaTyrlGlyHIsPheGlyArgAspAspAlaAs 122
210 CTTCACCTGCGAGGTGTCAGCCCC 234
|||||
122 pPheHrTrpGIuValIaIySpro 130

seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-312-544-5922

seq_documentation_block:
; Sequence 5922, Application US/60312544
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)A
; CURRENT APPLICATION NUMBER: US/60/312,544
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 10730
; SEQ ID NO 5922
; LENGTH: 143
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
US-60-312-544-8313

seq_documentation_block:
; Sequence 8313, Application US/60312544
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)A
; CURRENT APPLICATION NUMBER: US/60/312,544
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 10730
; SEQ ID NO 8313
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
US-60-312-544-8313

alignment_scores:
Quality: 127.00      Length: 25
Ratio: 5.292        Gaps: 0
Percent Similarity: 96.000      Percent Identity: 96.000

alignment_block:
US-09-198-779B-1 x US-60-312-544-8313 ..

Align seg 1/1 to: US-60-312-544-8313 from: 1 to: 138

160 AGGTCATCATAGAGCCGCGCATATAGCGCACTTGGCCGTGAGACGCCGA 209
|||||
106 ArgpheiIeIyStHrAlaIaIaTyrlGlyHIsPheGlyArgAspAspAlaAs 122
210 CTTCACCTGCGAGGTGTCAGCCCC 234
|||||
122 pPheHrTrpGIuValIaIySpro 130
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alignment_scores:

Quality: 127.00 Length: 25
Ratio: 5.292 Gaps: 0
Percent Similarity: 96.000 Percent Identity: 96.000

alignment_block:

US-09-198-779b-1 x US-60-324-109-31671 ..

Align seg 1/1 to: US-60-324-109-31671 from: 1 to: 79

160 AGGTCATCATAGACCGCCGATACGGCCACTTTGGCCGTGACGACGCCGA 209
|||||
47 ArgpheiellisthrAlaIatYrGlyHISpneGlyArgAspAspAlaAs 63
210 CTTCACTGCGAGGTGTCACGCC 234
|||||
63 pPheHrTrpGluValIValIysPro 71

seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-324-109-18261

seq_documentation_block:

; Sequence 18261, Application US/60324109
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)B
; CURRENT APPLICATION NUMBER: US/60/324,109
; NUMBER OF SEQ ID NOS: 2001-09-21
; SEQ ID NO 18261
; LENGTH: 82
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
US-60-324-109-18261

alignment_scores:

Quality: 127.00 Length: 25
Ratio: 5.292 Gaps: 0
Percent Similarity: 96.000 Percent Identity: 96.000

alignment_block:

US-09-198-779b-1 x US-60-324-109-18261 ..

Align seg 1/1 to: US-60-324-109-18261 from: 1 to: 82

160 AGGTCATCATAGACCGCCGATACGGCCACTTTGGCCGTGACGACGCCGA 209
|||||
52 ArgpheiellisthrAlaIatYrGlyHISpneGlyArgAspAspAlaAs 68
210 CTTCACTGCGAGGTGTCACGCC 234
|||||
68 pPheHrTrpGluValIValIysPro 76

seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-324-109-27080

seq_documentation_block:

; Sequence 27080, Application US/60324109
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)B

; CURRENT APPLICATION NUMBER: US/60/324,109

; CURRENT FILING DATE: 2001-09-21

; NUMBER OF SEQ ID NOS: 33196

; SEQ ID NO 27080

; LENGTH: 90

; TYPE: PRT

; ORGANISM: Zea mays subsp. mexicana

; FEATURE:
US-60-324-109-27080

alignment_scores:

Quality: 127.00 Length: 25
Ratio: 5.292 Gaps: 0
Percent Similarity: 96.000 Percent Identity: 96.000

alignment_block:

US-09-198-779b-1 x US-60-324-109-27080 ..

Align seg 1/1 to: US-60-324-109-27080 from: 1 to: 90

160 AGGTCATCATAGACCGCCGATACGGCCACTTTGGCCGTGACGACGCCGA 209
|||||
58 ArgpheiellisthrAlaIatYrGlyHISpneGlyArgAspAspAlaAs 74
210 CTTCACTGCGAGGTGTCACGCC 234
|||||
74 pPheHrTrpGluValIValIysPro 82

seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-324-109-17432

seq_documentation_block:

; Sequence 17432, Application US/60324109
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Stein, Joshua
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-10(52726)B
; CURRENT APPLICATION NUMBER: US/60/324,109
; CURRENT FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 33196
; SEQ ID NO 17432
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
US-60-324-109-17432

alignment_scores:

Quality: 127.00 Length: 25
Ratio: 5.292 Gaps: 0
Percent Similarity: 96.000 Percent Identity: 96.000

alignment_block:

US-09-198-779b-1 x US-60-324-109-17432 ..

Align seg 1/1 to: US-60-324-109-17432 from: 1 to: 92

160 AGGTCATCATAGACCGCCGATACGGCCACTTTGGCCGTGACGACGCCGA 209
|||||
60 ArgpheiellisthrAlaIatYrGlyHISpneGlyArgAspAspAlaAs 76
210 CTTCACTGCGAGGTGTCACGCC 234
|||||
76 pPheHrTrpGluValIValIysPro 84

seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-324-109-28766

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Date: Aug 20, 2002 2:49 AM

About: Results were produced by the Gencore software, version 4.5,
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Command line parameters:

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-GAOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPL=0.000
-LOOPEXT=0.000 -OGAOP=4.500 -OGAPEXT=0.050 -XGAOP=10.000
-XGAPEXT=0.500 -FGAOP=6.000 -FGAPEXT=7.000 -YGAOP=10.000
-YGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1
-MATRIX=biosum62 -TRANS=human40.cdi -LIST=45 -DOCALLIGN=200
-THR_SCORE=pcet -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pts -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USBR=US09198779.@CGN1_1_231 -NCPU=6 -ICPU=3 -LONGJOB
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPHY -WAIT -THREADS=1

Search information block:

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Query length: 235
Database: Pending_Patents_AA_Main.*
Database sequences: 3502263
Database length: 351980561
Search time (sec): 316.510000

score_list:

Sequence	Strd Orig	ZScore	EScore	Len	! Documentation	..
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/cgn2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-11671				127.00	323.28	3.0e-09
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/cgn2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-28766				127.00	320.13	3.0e-09
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/cgn2_6/ptodata/2/paa/US60.COMB.pep:US-09-708-427-50981				127.00	311.29	3.2e-09
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/cgn2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-17569				127.00	310.15	3.2e-09
/cgn2_6/ptodata/2/paa/US60.COMB.pep:US-60-324-109-17652				127.00	310.15	3.2e-09
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seq_documentation_block:

Sequence 9603, Application US/60312544
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jindong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)A
CURRENT APPLICATION NUMBER: US/60/312,544
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 10730
SEQ ID NO 9603
LENGTH: 48
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3205-165-H12_FLI
US-60-312-544-9603

alignment_scores:

Quality: 127.00 Length: 25
Ratio: 5.292 Gaps: 0
Percent Similarity: 96.000 Percent Identity: 96.000

alignment_block:

US-09-198-779b-1 x US-60-312-544-9603 ..
Align seg 1/1 to: US-60-312-544-9603 from: 1 to: 48

160 AGCTTCATCAGACCGCCGATAGCGCCATTGGCCGTGACGACCGCA 209
|||||||
16 ATGpHeiIeIyThrAlaIaIyrcIyHspHeGlyArGAspAspAlaAs 32
210 CTTGACCGCGCGAGGCGTCAACGCC 234
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32 pHeIhTrIrpGluValValysPro 40

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seq_documentation_block:

Sequence 31671, Application US/60324109
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jindong
APPLICANT: Stein, Joshua
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)B
CURRENT APPLICATION NUMBER: US/60/324,109
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 33196
SEQ ID NO 31671
LENGTH: 79
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
US-60-324-109-31671

FEATURES	FT	source	1.1182	/organism='Hordeum vulgare'.
source	FT	Location/Qualifiers	1.1182	
BASE COUNT		253 a	368 c	331 g 230 t
ORIGIN				
Query Match				
Best Local Similarity	26.2%;	Score 61.6;	DB 6;	Length 1182;
Matches	88.2%;	Pred. No. 1e-07;		
	67;	Conservative	0;	Mismatches 9; Indels 0; Gaps 0;
OY	160	aggttcatacaagaccgcgcatacggccacttggcgtgacgacgaccgactcaactgc	219	
Db	1084	AGGTTCAATCAAGACAGCTGCTTATGTCACCTTGGCCCGCAGATGCCACTTCACTGG	1143	
OY	220	gaggtggtcaagccccc	235	
Db	1144	GAGGTGTGAAGCCCC	1159	
RESULT	4			
LOCUS	E14402	1182 bp	DNA	linear
DEFINITION	cDNA encoding S-adenosylmethionine synthetase.			PAT 28-JUL-1999
ACCESSION	E14402			
VERSION	E14402.1	GI:5709085		
KEYWORDS	JP 1997313186-A/1.			
SOURCE	Hordeum vulgare.			
ORGANISM	Hordeum vulgare			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
	Poideae; Triticeae; Hordeum.			
	1 (bases 1 to 1182)			
REFERENCE	MORI,S.			
AUTHORS	GENE OF S-ADENOSYLMETHIONINE SYNTHASE			
TITLE	Patent: JP 1997313186-A 1 09-DEC-1997;			
JOURNAL	NIPPON OIL CO LTD			
COMMENT	OS Hordeum vulgare			
	PN JP 1997313186-A/1			
	PD 09-DEC-1997			
	PF 28-MAY-1996 JP 1996133406			
	PI MORI SATOSHI			
	PC C12N15/09,C07H21/04,C12N9/00//A01H1/00,A01H5/00; CC			
	strandedness: Double;			
	CC topology: Linear;			
	CC hypothetical: No;			
	CC anti-sense: No;			
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	FT	source	1.1182	
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source			1.1182	
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BASE COUNT		253 a	372 c	324 g 233 t
ORIGIN				
Query Match				
Best Local Similarity	26.0%;	Score 61;	DB 6;	Length 1182;
Matches	87.0%;	Pred. No. 1.6e-07;		
	67;	Conservative	0;	Mismatches 10; Indels 0; Gaps 0;
OY	159	caggttcatacaagaccgcgcatacggccacttggcgtgacgacgaccgactcaactgc	218	
Db	1083	CAGGTCATCAAGACAGCTGCTTACGTCACCTTGGCCGCATGATGCTGACTTCACTCG	1142	
OY	219	cgaagtggtcaagcccc	235	
Db	1143	GGAGTGTGAAGCCCC	1159	

[illegible]

Best Local Similarity	83.1%	Pred. No. 4,36-06;			
Matches	64;	Conservative	0;	Mismatches	13;
				Indels	0;
				Gaps	0;
Oy	159	caggttcataagaccgcgcatacagccacttggccgtgtacagcgcgacttacctg	218		
Db	1209	CCGGTTCATCAAGACCGCGCGGTACGCCCATTTCCGCCGCGAGATCCCGACTTCACATG	1268		
Oy	219	cgaagtggtcaagcccc	235		
Db	1269	GGAGGTTGTCAAGCCGC	1285		
RESULT	9				
LOCUS	AP003211/c				
DEFINITION	AP003211	150641 bp	DNA	linear	HTG 21-FEB-2001
	Oryza sativa chromosome 1 clone OSJNBa0011P19, *** SEQUENCING IN				
ACCESSION	AP003211				
VERSION	AP003211.1	GI:13027241			
KEYWORDS	HTG; HTGS; PHASE2.				
SOURCE	Oryza sativa (cultivar: Nipponbare) DNA, clone: OSJNBa0011P19.				
ORGANISM	Oryza sativa				
	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
	Ehrhartoideae; Oryzaceae; Oryza.				
	1 (sites)				
REFERENCE	Sasaki,T., Matsumoto,T. and Yamamoto,K.				
AUTHORS	Oryza sativa nipponbare(GM3) genomic DNA, chromosome 1, BAC				
TITLE	clone:OSJNBa0011P19				
JOURNAL	Published only in Database (2001) In press				
REFERENCE	2 (bases 1 to 150641)				
AUTHORS	Sasaki,T., Matsumoto,T. and Yamamoto,K.				
TITLE	Direct Submission				
JOURNAL	Submitted (19-FEB-2001) Takuji Sasaki, National Institute of				
	Agrrobiological Resources, Rice Genome Research program; Kannonnai				
	2-1-2, Tsukuba, Ibaraki 305-8602, Japan				
	(E-mail:tsasaki@ab.affrc.go.jp, URL:http://rgrp.dna.affrc.go.jp/,				
	Tel:81-298-38-7441, Fax:81-298-38-7468)				
COMMENT	NOTE: It currently consists of 1 contigs. Gaps between the contigs				
	are represented as runs of N. The order of the pieces is believed				
	to be correct as given, however the sizes of the gaps between them				
	are based on estimates that have provided by the submitter. This				
	sequence will be replaced by the finished sequence as soon as it is				
	available and the accession number will be preserved.				
	* NOTE: This is a 'working draft' sequence.				
	* This sequence will be replaced				
	* by the finished sequence as soon as it is available and				
	* the accession number will be preserved.				
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SOURCE	1..150641				
	/organism="Oryza sativa"				
	/cultivar="Nipponbare"				
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	/clone="OSJNBa0011P19"				
BASE COUNT	41696 a 33905 c 33240 g 41500 t	300	others		
ORIGIN					
Query Match	23.9%;	Score 56.2;	DB 2;	Length 150641;	
Best Local Similarity	83.1%;	Pred. No. 6,3e-06;			
Matches	64;	Conservative	0;	Mismatches	13;
				Indels	0;
				Gaps	0;
Oy	159	caggttcataagaccgcgcatacagccacttggccgtgtacagcgcgacttacctg	218		
Db	32940	CCGGTTCATCAAGACCGCGCGGTACGCCCATTTCCGCCGCGAGATCCCGACTTCACATG	32861		
Oy	219	cgaagtggtcaagcccc	235		
Db	32880	GGAGGTTGTCAAGCCGC	32864		
RESULT	10				

LOCUS	AY039010	545 bp	mRNA	linear	PLN 16-JUL-2001
DEFINITION	Elaeis oleifera S-adenosyl methionine synthetase (SAMS1) mRNA, partial cds.				
ACCESSION	AY039010				
VERSION	AY039010.1 GI:14764475				
KEYWORDS					
SOURCE	Elaeis oleifera.				
ORGANISM	Elaeis oleifera. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Arecaeae; Arecoideae; Coccoae; Elaeidinae; Elaeis.				
REFERENCE	1 (bases 1 to 545) Bhore,S.J. and Shah,F.H.				
AUTHORS	Isolation of S-adenosyl-L-methionine synthetase (SAMS1) cDNA clone from oil palm (Elaeis oleifera) mesocarp tissue				
TITLE	Unpublished				
JOURNAL	2 (bases 1 to 545)				
REFERENCE	Bhore,S.J. and Shah,F.H.				
AUTHORS	Direct Submission				
TITLE	Submitted (07-JUN-2001) School of Bioscience and Biotechnology, Faculty of Science and Technology, National University of Malaysia, 43600 Bangi, Selangor, Malaysia				
JOURNAL	Location/Qualifiers				
FEATURES	1..545				
source	/organism="Elaeis oleifera"				
gene	/db_xref="taxon:80265"				
CDS	<1..545				
	/gene="SAMS1"				
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	/gene="SAMS1"				
	/codon_start=3				
	/product="S-adenosyl methionine synthetase"				
	/protein_id="AAK72126.1"				
	/db_xref="GI:14764476"				
	/translation="EPLSVFDYTGCTGKIPDKELIKVENFDFRPGMIINIDLRKGNGRFLTAAIGHGRDDTDETVVAVPLGKPPAA"				
BASE COUNT	151 a 110 c 131 g 153 t				
ORIGIN					
Query Match	23.2%; Score 54.6; DB 8; Length 545;				
Best Local Similarity	81.8%; Pred. No. 1.2e-05;				
Matches	63; Conservative 0; Mismatches 14; Indels 0; Gaps 0;				
QY	159 caggttcacaaagccgcgcacatacgccacttgccgtgacgacgcgcacttcacctg 218				
DB	143 CAGGTTCCGAGACAGACAGCGCTTACGGGCGATTTCGGCAGGATGACACCACTTCACCTG 202				
QY	219 cgagtggtgtaagcccc 235				
DB	203 GGAGGTGTGAAGCCCC 219				
RESULT 11					
LOCUS	ACU17241 1272 bp mRNA linear PLN 03-MAY-2000				
DEFINITION	Actinidia chinensis S-adenosylmethionine synthetase mRNA, partial cds.				
ACCESSION	U17241				
VERSION	U17241.1 GI:726031				
KEYWORDS	S-adenosylmethionine synthetase.				
SOURCE	Actinidia chinensis.				
ORGANISM	Actinidia chinensis Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; Ericales; Actinidiaceae; Actinidia.				
REFERENCE	1 (bases 1 to 1272)				
AUTHORS	Whittaker,D.J., Smith,G.S. and Gardner,R.C.				
TITLE	Three cDNAs encoding S-adenosyl-L-methionine synthetase from Actinidia chinensis				
JOURNAL	Plant Physiol. 108 (3), 1307-1308 (1995)				
MEDLINE	95357424				

LOCUS	DINCARA	1632 bp	mRNA	linear	PIN 03-MAR-1994
DEFINITION	D.caryophyllus S-adenosylmethionine synthetase (CARSAM2) mRNA,				
ACCESSION	M61882				complete cds.
VERSION	M61882.1	GI:167961			
KEYWORDS	S-adenosylmethionine synthetase.				
SOURCE	D.caryophyllus petal, cDNA to mRNA, clone pSAM2.				
ORGANISM	Dianthus caryophyllus				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
TITLE	Caryophyllidae; Caryophyllales; Caryophyllaceae; Dianthus.				
JOURNAL	larsen,P.B. and Woodson,W.R.				
FEATURES	Cloning and nucleotide sequence of a s'-adenosylmethionine				
source	synthetase cDNA clone from carnation				
gene	Plant Physiol. (1991). In press				
CDs	Location/Qualifiers				
	1..1632				
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	72..1262				
	/gene="CARSAM2"				
	/codon_start=1				
	/product="S-adenosylmethionine synthetase"				
	/protein_id="AA033274.1"				
	/db_xref="GI:304637"				
	/translation="MAAADPFLTFSVNEGHPDKIDDISAVIDLACLAQDAESV				
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	KNGICAMLRPDGKTQVTVEYNENGAWPIRVHVLISTGHDETVAIDEIADLKEHV				
	IKVPILPERKYIDENTIFHLINPSGREVIGAGDGALGTGRKIIIDRYGGMAHGGAFFR				
	KDPKPVDSGAVIARAOKASIVASGLARRCIVOISVIGPEPLSVFDVPGTGKTD				
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	KPKQA"				
BASE COUNT	405 a	383 c	424 g	420 t	
ORIGIN					
Query Match	21.8%; Score 51.2; DB 8; Length 1632;				
Best Local Similarity	53.0%; Pred. No. 0.00013;				
Matches	62; Conservative	0; Mismatches	55; Indels	0; Gaps	0;
QY	119 gtlnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncagggttcataagaccgcg	178			
Db	1120 GTATGATGCCATTGCCTCGCACTCAAGAAGGGTGGGACACGTTACTTGAGACAGCCG	1179			
QY	179 catcggccactcttgccgcyaacgacgccgaattcacctcgagagtgtgtaagcccc	235			
Db	1180 CGTAGTGACACTTGTGACGTGAAGACC GCCGACTCACGTGGGAGCGTCGAAGACC	1236			
RESULT	17				
LOCUS	OSA296743	1594 bp	mRNA	linear	PLN 10-DEC-2001
DEFINITION	Oryza sativa mRNA for s'-adenosylmethionine synthetase (SAMS gene).				
ACCESSION	AJ296743				
VERSION	AJ296743.1	GI:17529620			
KEYWORDS	S-adenosylmethionine synthetase; SAMS gene.				
SOURCE	Oryza sativa.				
ORGANISM	Oryza sativa				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
AUTHORS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;				
TITLE	Ehrhartoidesae; Oryzaceae; Oryza.				
JOURNAL	1 (sites)				
REFERENCE	Mukhopadhyay,A., Sharma,S. and Tyagi,A.K.				
AUTHORS	Isolation and characterization of a new member of the rice				
REFERENCE	S-adenosyl-L-methionine synthetase family				
AUTHORS	unpublished				
TITLE	2 (bases 1 to 1594)				
TITLE	Tyagi,A.K.				
TITLE	Direct Submission				

JOURNAL	Submitted (21-AUG-2000) Tyagi A.K., Department of Plant Molecular Biology, University of Delhi South Campus, Benito Juarez Road, New-Delhi, INDIA									
FEATURES	Location/Qualifiers									
source	1..1594									
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	/variety="Pusa Basmati 1"									
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	/tissue_11b="Root"									
gene	108..1298									
	/gene="SAMS"									
CDS	108..1298									
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	/EC_number="2.5.1.6"									
	/codon_start=1									
	/product="S-adenosylmethionine synthetase"									
	/protein_id="CAC82203.1"									
	/db_xref="GI:17529621"									
	/translation="MAADPTLPTSESNEGHPPDKLCDQSDAVIDACLAEDPSKYAA CECTKIKMVMVFGELITTKAVDYELIVRETCRNIGVSAVDGLADHCKVLNIEQD SPDIAQVGHGHTKRPDEIIGADQGHMGVATDETPELMPLSHVLATKARLKVKK NGTCMLRPDGKTKQTVLVEYRNESGARVPVHVLISQHDETVINDEIADLKEHVIT KPVIEQSLDEKTIIFHLNPSGRFVYGPBGAGLGRKLIIDTVGGMGAGHGGAFSKK DPTVDRSGAYVARQAASTVASGLARCIYQVSYAIGVPEPLSPVDIYGTGTGIPPK ELIKVKNPDPFRGMIIINIDLKKGNGRILTKAAIGHREDDPDTWEYVKPLKWE KPSA									
BASE COUNT	374	a	433	c	406	g	381	t		
ORIGIN										
Query Match	21.7%; Score 51; DB 8; Length 1594;									
Best Local Similarity	80.0%; Pred. No. 0.00015;									
Matches	60;	Conservative	0;	Mismatches	15;	Indels	0;	Gaps	0;	
OY	161	gggtcatcaagccgcgcgcatagcgcacattggcgcgtgacgacgcgactcaccttcg	220							
	1		1		1		1		1	
Db	1198	gctactctcaagcggcgcttaccgcttaccgacttcggaaggacagaccagacttacctggg	1257							
OY	221	agggtggtcaagcccc	235							
	1		1		1		1		1	
Db	1258	aggtggtgaagcccc	1272							
RESULT	18									
LOCUS	OSASMS1	2183	bp	DNA	linear	PLN 06-DEC-1994				
DEFINITION	O.sativa (PRSAM-1) gene for S-adenosyl methionine synthetase.									
ACCESSION	Z26867									
VERSION	Z26867.1 GI:450548									
KEYWORDS	S-adenosylmethionine synthetase.									
SOURCE	Oryza sativa.									
ORGANISM	Oryza sativa									
	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehretidae; Oryzae; Oryza.									
REFERENCE	1 (bases 1 to 2182)									
AUTHORS	Van Breusegem,F., Dekeyser,R., Gielens,J., Van Montagu,M. and Caplan,A.									
TITLE	Characterization of a S-adenosylmethionine synthetase gene in rice									
JOURNML	Plant Physiol. 105 (4), 1463-1464 (1994)									
MEDLINE	95062735									
REFERENCE	2 (bases 1 to 2183)									
AUTHORS	Van Breusegem,F.									
TITLE	Direct Submission									
JOURNML	Submitted (08-OCT-1993) Van Breusegem F., Universiteit Gent, Labo voor Genetika, Ledeganckstraat 35, Gent, Belgium, 9000									
REMARK	revised by [3]									
REFERENCE	3 (bases 1 to 2183)									
AUTHORS	Van Breusegem,F.									
TITLE	Direct Submission									
JOURNML	Submitted (25-JAN-1994) Van Breusegem F., Universiteit Gent, Labo voor Genetika, Ledeganckstraat 35, Gent, Belgium, 9000									
COMMENT	On Jan 26, 1994 this sequence version replaced gi:407153.									

Location/Qualifiers
1. .2183

FEATURES	source
16766:	contig of 16766 bp in length
16767	16866: gap of unknown length
16867	91884: contig of 75018 bp in length
91885	91984: gap of unknown length
91985	120829: contig of 2845 bp in length
120830	120929: gap of unknown length
120930	150934: contig of 30025 bp in length
120934	Location/Qualifiers
1.	.150954

BASE COUNT
ORIGIN

	BASE COUNT	43594	a	32703	c	30779	g	43569	t	309	others
	ORIGIN										
Query Match		21.7%		Score 51;		DR 2;		Length 150954;			
Best Local Similarity		80.0%		Pred. No. 0.00022;							
Matches 60;	Conservative	0;	Mismatches 15;	Indels 0;	Gaps						
Oy	161	gtttcatcaagacgcgcgcatacggccacttggccgtgaagacgccgacttcacctgcg	220								
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21.7%; Score 51; DB 8; Length 2183;
80.08; Pred. No. 0.00016;

	DB	123662	AGGTGCTGAAGCCCC	123676	
RESULT	20				
LOCUS	AY061895				
DEFINITION	Arabidopsis thaliana ATlg02500/Tt14P4_22 mRNA, complete cds.	1107 bp	mRNA	linear	PLN 19-NOV-2001
ACCESSION	AY061895				
VERSION	AT061895.1	GI:16974436			
KEYWORDS	FLI_CDNA.				
SOURCE	thale cress.				

LOCUS	AC087552	150954 bp	DNA	linear	HTG: 28-AUG-2001
DEFINITION	Oryza sativa chromosome 5 clone P0519E07, *** SEQUENCING IN PROGRESS ***, 4 ordered pieces.				
ACCESSION	AC087552				
VERSION	AC087552.2	GI:15320908			
KEYWORDS	HTG; HTGS PHASE3.				
SOURCE	Oryza sativa.				
ORGANISM	Oryza sativa				

-I.C., Chow, T.-Y., Wu, H.-P., Chao, Y.-T., Liu, S.-M.,

TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Lee, P.-F., Su, C.-L., Chen, C.-S. and Shaw, J.-F.		Oryza sativa PAC P0519E07 genomic sequence				
Unpublished		2 (bases 1 to 150954)				
Hsing, Y.-I.C. and Chow, T.-Y.						
Direct Submission						
Submitted (09-JAN-2001)	Institute of Botany, Academia Sinica,	128,				
Section 2, Yien-chu-yuan Road, Nankang, Taipei 11529, Taiwan						
On Aug 26, 2001 this sequence version replaced gi:12056977.						

COMMENT

* the accession number will be preserved.
* by the finished sequence as soon as it is available and
* This sequence will be replaced
* provided by the submittor.
* of the gaps between them are based on estimates that have
* the accession number will be preserved.

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 1107)

Klm,C.J., Chen,H., Cheuk,R., Koseema,E., Meyers,M.C., Bahh,J., Bowser,L., Carninci,P., Chang,E., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y., Ishida,J., Jones,T., Kamitaya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quech,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C., Totlunt,M., Wu,H.C., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.

Arabidopsis ORF clones

REFERENCE AUTHORS

TITLE
JOURNAL
Submitted (30-OCT-2001) Salk Institute Genomic Analysis Laboratory
Direct Submission

COMMENT

collection and clustering of RAFL CNAs (RAFL cDNA : 'RIEN Arabidopsis Full-length cDNA') : Seki, M., Natsumasa, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawa, J., Hayashizaki, Y. and Shinozaki, K.

LOCUS	AY052311	1459 bp	mRNA	linear	PLN 05-SEP-2001
DEFINITION	Arabidopsis thaliana At1g02500/T14P_22 mRNA, complete cds.				
ACCESSION	AY052311				
VERSION	AY052311.1 GI:15450420				
KEYWORDS	FLI CDNA.				
SOURCE	thale cress.				
ORGANISM	Arabidopsis thaliana				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
AUTHORS	1 (bases 1 to 1459)				
TITLE	Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Dale, U.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamuya, A., Kallin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.				
JOURNAL	Arabidopsis CDNA clones				
REFERENCE	Unpublished				
AUTHORS	2 (bases 1 to 1459)				
TITLE	Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Dale, U.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamuya, A., Kallin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.				
JOURNAL	Direct Submission				
REFERENCE	Submitted (17-AUG-2001) Salk Institute Genomic Analysis Laboratory (SIGnAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA				
COMMENT	RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL CDNA: 'RIKEN Arabidopsis Full-length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamuya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.				
TITLE	The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J., Bowser, L., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Jones, T., Kallin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.				
FEATURES	Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.				
SOURCE	Location/Qualifiers				
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	203..1309				
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	/protein_id="AAK96504.1"				
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	3' UTR	399 a	354 c	336 g	370 t	
	BASE COUNT					
	ORIGIN					
	Query Match	21.4%	Score 50.4;	DB 8:	Length 1459;	
	Best Local Similarity	78.9%;	Pred. No. 0.00023;			
	Matches	60; Conservative	0; Mismatches	16;	Indels	0; Gaps
OY	160 aggttcataagacgcgcgcatcggccacttgcgccttgacgacgcgcgaattcacccgc	219				
Db	1208 AGGTTCTTGAAGAACTCGCCGCTTACGGACACTTTGGAGAAGACGACCCTGCATTCACTCG	1267				
OY	220 gaagtgtcaagcccc	235				
Db	1268 GAAGTCGTCAAGCCAC	1283				
RESULT	23 AF325061	1508 bp	mRNA	linear	PLN 23-MAY-2001	
LOCUS	AF325061					
DEFINITION	Arabidopsis thaliana Atlg02500 (Atlg02500/T14P4_22)				mRNA, complete cds.	
ACCESSION	AF325061					
VERSION	AF325061.2					
KEYWORDS	FLI CDNA.					
SOURCE	thale cress.					
ORGANISM	Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids. 1 (bases 1 to 1508) 2 (bases 1 to 1508)					
REFERENCE	AUTHORS					
JOURNAL	Shim,P., Chao,Q., Brooks,S., Chen,H., Cheuk,R., Johnson-Hopson,C., Khan,S., Kim,C.J., Banh,J., Bowser,L., Chung,M.K., Goldsmith,A.D., Jones,T., Karlin-Neumann,G., Lam,B., Lee,U.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M., Palm,C.J., Pham,P.K., Quach,H.L., Sakano,H., Southwick,A., Toriumi,M., Yamada,K., Yu,G., Davis,R.W., Theologis,A. and Ecker,J.R. Arabidopsis cdna clones Unpublished					
REFERENCE	AUTHORS					
JOURNAL	Shim,P., Chao,Q., Brooks,S., Chen,H., Cheuk,R., Johnson-Hopson,C., Khan,S., Kim,C.J., Banh,J., Bowser,L., Chung,M.K., Goldsmith,A.D., Jones,T., Karlin-Neumann,G., Lam,B., Lee,U.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M., Palm,C.J., Pham,P.K., Quach,H.L., Sakano,H., Southwick,A., Toriumi,M., Yamada,K., Yu,G., Davis,R.W., Theologis,A. and Ecker,J.R. Direct Submission Submitted (30-NOV-2000) Salk Institute Genomic Analysis Laboratory (SIGnAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA 3 (bases 1 to 1508)					
REFERENCE	AUTHORS					
JOURNAL	Shim,P., Chao,Q., Brooks,S., Chen,H., Cheuk,R., Johnson-Hopson,C., Khan,S., Kim,C.J., Banh,J., Bowser,L., Chung,M.K., Goldsmith,A.D., Jones,T., Karlin-Neumann,G., Lam,B., Lee,U.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M., Palm,C.J., Pham,P.K., Quach,H.L., Sakano,H., Southwick,A., Toriumi,M., Yamada,K., Yu,G., Davis,R.W., Theologis,A. and Ecker,J.R. Direct Submission Submitted (16-MAR-2001) Salk Institute Genomic Analysis Laboratory (SIGnAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA On Mar 16, 2001 this sequence version replaced gi:11762285. RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shimozaki,K.					
COMMENT						

Oy	220	gaagtggtcaagcccc	235			
Db	1227	GAGTACTCAGCCAC	1242			
RESULT	25	AB022216/c				
LOCUS		AB022216	80167 bp	DNA	linear	PLN 27-DEC-2000
DEFINITION		Arabidopsis thaliana genomic DNA, chromosome 3, PI clone: MGD8.				
ACCESSION		AB022216	BA000014			
VERSION		AB022216.1	GI:4159705			
KEYWORDS		Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui P1 clone:MGD8.				
ORGANISM		Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.				
REFERENCE		Sato, S., Nakamura, Y., Kaneko, T., Katoh, T., Asamizu, E. and Tabata, S. Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty P1 and YAC clones				
AUTHORS		Sato, S., Nakamura, Y., Kaneko, T., Katoh, T., Asamizu, E. and Tabata, S.				
TITLE		1 (sites)				
JOURNAL		DNA Res. 7 (2), 131-135 (2000)				
MEDLINE		20277480				
REFERENCE		2 (bases 1 to 80167)				
AUTHORS		Sato, S., Nakamura, Y., Kaneko, T., Kato, T., Asamizu, E. and Tabata, S.				
TITLE		Direct Submission				
JOURNAL		Submitted (08-JAN-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamuekazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)				
COMMENT		Address for correspondence: kaos@kazusa.or.jp For the latest information on annotation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/aggd.graph.cgi?c=MGD8 Genes with similarity to proteins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein'. The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, http://compbio.ornl.gov/Grail-1.3/), NetScan (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html), NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and SplicePredictor (Volker Brendel, Stanford University, http://gremmit.zool.iastate.edu/cgi-bin/sp.cgi). Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan-SE/). This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is MCE21 and the 3' clone is MTO12.				
FEATURES		Location/Qualifiers				
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		/evidence=not_experimental				
		/product="13pamide dehydrogenase"				
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 SCDNKILTYDFELFRSPAYSLDKESKFLKADFPFKNYLLEFSPQNDQIAYLSVVR
 QEKALAQDRDPTSSIKMNIWYTKTKIDADDLSMNSFLVDFGKVLTLSEPLFVLVD
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 complement(23448..23835)
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 CNGFLCATMNCRLVWNPCTGQITWIIIPTRDSDDIVALGGDDKSSLSHSLYKILR
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DEFINITION	Arabidopsis thaliana chromosome I BAC T14P4 genomic sequence, complete sequence.		PLN 06-SEP-2000
ACCESSION	AC022521		
VERSION	AC022521.4	GI:7958958	
KEYWORDS	HTG.		
SOURCE	thale cress.		
ORGANISM	Arabidopsis thaliana		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons: core eudicots; Rosidae: eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
AUTHORS	1 (bases 1 to 121668) Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Nguyen,M., Lam,B., Southwick,A., Miranda,M., Brooks,S., Buchler,E., Hwang,B., Chou,J., Choi,E., Gonzalez,A., Gonzalez,A., Hwang,B., Johnson-Hopson,C., Khar,S., Kim,C., Koo,T., Lee,J.M., Lenz,C., Liu,A., Liu,K., Liu,S., Mukharsky,N., Pham,P., Sakano,H., Schwartz,J., Shinn,P., Thaverl,A., Toriumi,M., Vaysberg,M., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.		
JOURNAL	2 (bases 1 to 121668) Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Nguyen,M., Lam,B., Southwick,A., Bei,Q., Buchler,E., Chin,C., Chou,J., Choi,E., Dunn,P., Gonzalez,A., Hwang,B., Kim,C., Koo,T., Lee,J.M., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S., Mukharsky,N., Pham,P., Sakano,H., Schwartz,J., Shinn,P., Thaverl,A., Toriumi,M., Vaysberg,M., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.		
REFERENCE	Submitted (05-FEB-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA		
AUTHORS	3 (bases 1 to 121668) Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Nguyen,M., Lam,B., Southwick,A., Bei,Q., Buchler,E., Chin,C., Chou,J., Choi,E., Dunn,P., Gonzalez,A., Hwang,B., Kim,C., Koo,T., Lee,J.M., Lenz,C., Li,J., Liu,A., Liu,K., Liu,S., Mukharsky,N., Pham,P., Sakano,H., Schwartz,J., Shinn,P., Thaverl,A., Toriumi,M., Vaysberg,M., Walker,M., Yu,G., Ecker,J., Theologis,A. and Davis,R.W.		
JOURNAL	Direct Submission Submitted (15-MAR-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA		
REFERENCE	4 (bases 1 to 121668) Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A. and Davis,R.W.		
AUTHORS	Direct Submission Submitted (20-MAY-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA		
JOURNAL	5 (bases 1 to 121668) Federspiel,N.A., Palm,C.J., Conway,A.B., Conn,L., Hansen,N.F., Altafi,H., Nguyen,M., Lam,B., Southwick,A., Ecker,J., Theologis,A. and Davis,R.W.		
REFERENCE	Direct Submission Submitted (06-SEP-2000) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA		
AUTHORS	On May 20, 2000 this sequence version replaced gi:7243863. Bases 1-75,600 of clone T14P4 overlap with bases 74,643-100,239 of BAC Clone F22D16 (AC009525). e-mail for correspondence: arabseq@stanford.edu Genes with similarity to proteins in the databases are named 'putative', '-like' or 'similar to'. Genes that have EST similarity but no significant protein similarity are described as 'unknown proteins'. Genes that are annotated based only on gene		
COMMENT			

prediction software are described as 'hypothetical proteins'. The gene prediction programs used to predict genes include: Graal (Informatics Group, Oak Ridge National Laboratory, <http://compbio.ornl.gov/section/index.html>), GENSCAN (Chris Burge, <http://genes.mit.edu/GENSCAN/>), EXA (Victor Solovyev, <http://genomic.sanger.ac.uk/gf/gf.shtml>), and NetPlantGene (S.M. Hebsgaard, et al., CBS, Technical University of Denmark, <http://www.cbs.dtu.dk/NetPlantGene.html>).

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Matches 60; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

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QY 220 gaagtgtagaagcccc 235

Db 97661 GAACTGCTCAAGCCAC 97646

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RESULT 27
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LOCUS
DEFINITION Petunia x hybrida S-adenosyl-L-methionine synthetase mRNA, complete cds.
ACCESSION AF170798
VERSION AF170798.1
KEYWORDS GI:5726593
SOURCE
ORGANISM petunia x hybrida.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Astidae; eusterids I; Solanales; Solanaceae; Petunia.
1 (bases 1 to 1539)
REFERENCE Soong,S.C. and to,K.Y.
AUTHORS Nucleotide Sequence Of A cDNA (AF170798) Encoding Type I
TITLE S-Adenosyl-L-Methionine Synthetase From Petunia hybrida.
JOURNAL Plant Physiol. 121 (3), 1053 (1999)
REFERENCE 2 (bases 1 to 1539)
AUTHORS To,K.Y. and Sung,H.C.
TITLE Direct Submission
JOURNAL Submitted (21-JUL-1999) Institute of Biocgricultural Sciences,
Academia Sinica, Taipei 11529, Taiwan
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REFERENCE 1 (bases 1 to 1665)
AUTHORS Cheuk,R., Chen,H., Kim,C.J., Meyers,M.C., Shinn,P., Banh,J.,
Bowler,L., Carninci,P., Chung,M.K., Goldsmith,A.D., Hayashizaki,Y.,
Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J.,
Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Narusaka,M.,
Nguyen,M., Palm,C.J., Pham,P.K., Quach,H.L., Sakano,H., Sakurai,T.,
Satou,M., Seki,M., Southwick,A., Toriumi,M., Yamada,K., Yu,G.,
Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.
TITLE Arabidopsis cDNA clones
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1665)
AUTHORS Cheuk,R., Chen,H., Kim,C.J., Meyers,M.C., Shinn,P., Banh,J.,
Bowler,L., Carninci,P., Chung,M.K., Goldsmith,A.D., Hayashizaki,Y.,
Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J.,
Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Narusaka,M.,
Nguyen,M., Palm,C.J., Pham,P.K., Quach,H.L., Sakano,H., Sakurai,T.,
Satou,M., Seki,M., Southwick,A., Toriumi,M., Yamada,K., Yu,G.,
Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2001) Salk Institute Genomic Analysis Laboratory
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
USA
COMMENT The Salk, Stanford, PEGC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs (Shinn,P., Chen,H.,
Cheuk,R., Kim,C.J., Koesema,E., Meyers,M.C., Tracy,S.E., Banh,J.,
Bowler,L., Chung,M.K., Goldsmith,A.D., Jones,T., Karlin-Neumann,G.,
Lam,B., Lee,J.M., Lin,J., Liu,S.X., Miranda,M., Nguyen,M.,
Palm,C.J., Pham,P.K., Quach,H.L., Sakano,H., Southwick,A.,
Tang,C.C., Toriumi,M., Yamada,K., Yu,G., Davis,R.W., Theologis,A.,
and Ecker,J.R.
Shinn,P. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to
this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk)
contributed equally to this work as PIs.
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1327..1665
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Query Match 21.2%; Score 49.8; DB 8; Length 1665;
Best Local Similarity 77.9%; Pred. No. 0.00035;
Matches 60; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
Qy 159 caggttcacgaagccgcgcacattggccgctgacgacgcgcgacttaccctg 218
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Db 1233 CAGGTTCCAGAAACCGCTGCGTATGCCATTTCGGGCGTGATGACCCCTGACTTCACCTTG 1292

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DEFINITION	Arabidopsis thaliana chromosome II section 201 of 255 of the complete sequence. Sequence from clones T1f8.			
ACCESSION	AC006822	AE002093		
VERSION	AC006822.6	GI:6598638		
KEYWORDS	HTG.			
SOURCE	thale cress.			
ORGANISM	Arabidopsis thaliana			

REFERENCE
1 (bases 1 to 114950)

AUTHORS Lin, X., Kaul, S., Rounsley, S.D., Shree, T.P., Beilto, M.-I., Town, C.D., Fujii, C. Y., Mason, T.M., Bowman, C.L., Barnstead, M.E., Feldblum, T.V., Buell, C.R., Ketchum, K.A., Lee, J.-J., Ronning, C.M., Ko, H., Moffatt, K.S., Cronin, L.A., Shen, M., VanAken, S.E., Umayam, L., Tallon, L.J., Gill, J.E., Adams, M.D., Carrere, A.J., Crasay, T.H., Goodman, H.M., Somerville, C.R., Copenhaver, G.P., Preuss, D., Nierman, W.C., White, O., Eisen, J.A., Salzberg, S.L., Fraser, C.M. and Venter, J.C.

TITLE Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*

JOURNAL Nature 402 (6763), 761-768 (1999)

MEDLINE 20083487
 PUBMED 10617197
 REFERENCE 2 (bases 1 to 114950)
 AUTHORS Lin, X.
 JOURNAL Direct Submission
 TITLE Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
 Medical Center Dr., Rockville, MD 20850, USA
 COMMENT On Dec 17, 1999 this sequence version replaced gi:4883599.

On Dec 17, 1999 this sequence version replaced g1:4883599. The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (<http://www.tigr.org/fdb/a/t.html>).

Genes were identified by a combination of three methods: Gene prediction programs including GSNAIL (<http://arthur.epm.ornl.gov/pub/gsnail>), GeneFinder (Phil Green, University of Washington), GENSCAN (Chris Burge, <http://genome.stanford.edu/GENSCAN.html>), and NetPlantGene (<http://www.cbs.dtu.dk/services/NetPlantGene/>), searches of the complete sequence against a peptide database and plant EST databases at RIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>). Simple repeats were identified by RepeatMasker (Arjan Smit, <http://ftp.genome.washington.edu/RM/RepeatMasker.html>). Genes are numbered from the top to bottom of the chromosome.

We thank the GSHL/MasNU/ABI consortium for sequencing BAC clones 66P23, F536, T17A5, and T13J16, the ESSA group for sequencing clones P13D3, and Scott Jackson, Jinting Jiang, Klaus Meyer, Eric Richards and Satoshi Tabata for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanli Khalak, Michael E. Heaney, Lily Fu, Feng Jiang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and

database support.

This work was supported by the National Science Foundation Department of Energy and the US Department of Agriculture.

Address all correspondence to: at@tlgr.org.

FEATURES

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complement(join(10880, .10967,11066, .11350,11467, .11788,
11871, .11976,12054, .12281,12393, .12546))
/gene="At2g36640"
/note="hypothetical protein"
/codon_start=1
/protein_id="AAD31570.1"
/db_xref="GI:4883601"
/translation="MGLSLDDVYIISQSEKEDPSYITINCEDRKGLGCDCLRIILFF
GIVATRGVSGIDGKCVLWVYIGKPTTNLLKMLVVASPFSWAFGISRCYLSOS
ISQPKPDLFLDLACSDRTGLGLDYETELVXLEINIEKVISITTPGKWMDFEYV

```

```

GHHSHGJITLWVNIADVNSJHJLHITCODHGLLOJLDMRPFKXFNJLSIGR
TILKXNNEIDLTVFVSDGRIILSSKXLLALRLEALGLOJLRYVMMNRPDRELLV
TNPVLSKSGRQVDFHJLALAKDKIDCFJSAIGHYVGDREWEVYVLLNEEDSLR
IPRKSIEEYKWTMGCE"
Complement(join(13665..14290,14445..14495,14614..14733,
14814..14916,15631..15590,15684..15642,16419..16581,
16696..16738,16900..17018,17437..17552,17834..17953,
18118..18241,195240..18805,18889..18964,19109..19243,
19336..19445,19848..19688,25019)..>25114))
"/gene="AT2g36850"
Complement(1336850..Complement(1336850..>25114)
"/gene="AT2g36850"
/notes="fl18.3"
Complement(join(13931..14290,14445..14495,14614..14733,
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16696..16738,16900..17018,17437..17552,17834..17953,
18118..18241,195240..18805,18889..18964,19109..19243,
19336..19445,19848..19688,25019..25114))
"/gene="AT2g36850"
/codon_start=1

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/product="putative glucan synthase"
/protein_id="AAD31571.1"
/db_xref="GI:483602"
/translation="MRTIPACELSLPMKTESRLSKPKRRKRVSEIDQKRLHLTL
VKDAANVPKLNLEARRLEFNTSLFMMPQAPVAEWPVSEFTPYSELYSSSE
LSENEDEISILFYLOKIFPEMEENTLGRSESTGADALDASTDALIELFWYSR
GOTLARVGMAYVRRALMLOSELERRGIGVDASLTNNRGFESSIARADAKFT
YVSCOIGQOQKQKRPATDITGILLOYEALRVAFHISEVNGDSSGGKREYSK
LYKADHGRDEIYSIKLPDPRKLEGRPENONNAIVTTRGAIQTIMNDNYLEEA
IKMRNLSEPHKHCIRKRPITLIGREHVFGRNMGHPDVFDRIFHITRGISKAS
RVINISEDIVAGMRNSTLRQGNITFHDVDGLNLTALFEGKVAAGNGOVLSDRYRI
GQLEDFEPMMSFYFTVGVYCTMAFSGADRAISNTALSGNTALDALNMOFLVIG
ITFVAVPMAGFLELGLKALFSEFTTMOFQCSVFTFSLGTRHFGRTLHGAKV
YLLIYIAMTVEDEEDVSMVMKGGVGYKGLSWMSEEEQAHOTLRGRTLEIIS
LRFEMFGYIVYKLDITPRKNTSLATXGSMVYIVYVLFEGVASITITALLIVAIAM
TDLSPDKFACVLCITPTGMAILLATITWKOVLRVLGLMEVREFGRYLDAMGMLIF
SPIALDSWEPSTFSTOSRLFNQAFSNGLESIILAGNANVET"
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/gene="At2g36860"
/product="L-RNA-Thr"
/anticondon=(pos:29206..29208,aa:thr)
complement(29158..29241)
/gene="At2g36860"
/nc="T1J8.4"
/rpl_family="r(TA)n"
complement(join(<31865..32231,32911..33128,33211..33311,
33413..>33626))
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complement(<31865..>33626)
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/nc="T1J8.5"
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33413..33626))
/gene="At2g36870"
/codon_start=1
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/protein_id="AAD31572.1"
/db_xref="GI:483603"
/translation="MGNLSLISLIFHLVIMGSSVNAVMPSPGYPSSKRVGLNLT
KGFRLNGPOHQRMDONALRTWLDRTSSGSKSRKPRSGTFGANIKLOPRTAGVIT
SLYSNNBAHFGFDEVDIEFLGTTFGKPYTLQNNVYIRGSDGKIIGREKRFALMD
PTKDFHHYALIMSPRELIPLVDIPIRRYPKKSASTPLRBMVLYGSIWDASVATD
GKXYADRYQPFETAKYTNFNALCTAVSASACYPDLASPSYRSGGLTRQOHQAMVQT
HSWVNYCKDYKRPKHSLSLPECMR"
complement(34064..34093)
/rpl_family="r(GAA)n"
38445..38519
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complement(join(<38717..39891,40252..40392))
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/gene="At2g36880"
/nc="T1J8.6"
complement(38717..39889)
/gene="At2g36880"
/codon_start=1
/product="putative s-adenosylmethionine synthetase"
/protein_id="AAD31573.1"
/db_xref="GI:483604"
/translation="METFLFTSSVNEGHDKLDOISDAILDACLEQDESKVACET
CTKTNMVGELTTAKVYERIVRSTCREIGFISADVGLDADKCVLAINIBOOSD
IAOGVHGLTKRPEDIGADQGHMFYATDEPELMPLTHTVLAATKLGAKLTVRKNT
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Query Match 21.2%: Score 49.8; DB 8; Length 114950;
Best Local Similarity 77.9%: Pred. No. 0.00049;
Matches 60; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 159 caggttcaacaagccgcatacgccacttggccgtgacagccgcgacttccactg 218
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 38810 CAGGTTCCAGAAACCGCTGCGTATGGCCATTTCGGCGGTGATGACCTTCACTTG 38751
QY 219 cgaggtgtgtaagcccc 235

DB 38750 GGAGTTGTCAAGCCGC 38734
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 30
AF443869
LOCUS AF443869 772 bp mRNA linear PLN 02-DEC-2001
DEFINITION Solanum tuberosum S-adenosylmethionine synthetase mRNA, partial
cds.
ACCESSION AF443869
VERSION AF443869.1 GI:17226671
KEYWORDS
SOURCE potato.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; easterids I; Solanales; Solanaceae; Solanum.

REFERENCE
AUTHORS Ambrosino, P., Bosco, A. and Ruocco, M.
TITLE S-adenosylmethionine synthetase from potato
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 772)
AUTHORS Ambrosino, P., Bosco, A. and Ruocco, M.
TITLE Direct Submission
JOURNAL Submitted (06-NOV-2001) At. Bo. Pa. Ve, University, Via Universite,
100, Portici, NA 80055, Italy
FEATURES
source location/Qualifiers
1..772
/organism="Solanum tuberosum"
/db_xref="taxon:4113"
<1..358
/codon_start=2
/product="S-adenosylmethionine synthetase"
/protein_id="AAL37899.1"
/db_xref="GI:17226672"
/translation="KDPTKVDSCAVYIVROAKSVASGLARRCIMOVSYAIGVAPPL
SAFVDYTKGIIIDKDLIVLIKFNFDPRGMSINDDLKGNRXXKTAIGHFGND
DPDTMETVYKLRKA"

CDS

BASE COUNT 199 a 140 c 165 g 264 t 4 others
ORIGIN

Query Match 20.8%: Score 48.8; DB 8; Length 772;
Best Local Similarity 76.6%: Pred. No. 0.00064;
Matches 59; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 159 caggttcaacaagccgcatacgccacttggccgtgacagccgcgacttccactg 218
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 265 CAGGTNCAGAAAGACTGACGCTTACGTCACCTTGGAGCTGATGACCCGATTTCACCTG 324

QY 219 cgaggtgtgtaagcccc 235
||| ||||| |||
DB 325 GGAGACTGTCAAGGTC 341

RESULT 31

LESLAMSGA 1479 bp mRNA linear PLN 12-MAY-1995
LOCUS LESLAMSGA
DEFINITION L.esculentum S-adenosyl-L-methionine synthetase mRNA, complete cds.
ACCESSION 224741
VERSION 224741.1 GI:429103
KEYWORDS S-adenosyl-L-methionine synthetase.
SOURCE tomato.

ORGANISM

Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterales; easterids I; Solanales; Solanaceae; Solanum;
Lycopersicon.
1 (bases 1 to 1479)
Espartero, J. and Pardo, J.M.
TITLE Differential expression of three S-adenosylmethionine synthetase
genes in response to stress in tomato
JOURNAL Unpublished

[illegible]

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/codon_start=1
/product="S-adenosyl-L-methionine synthetase"
/protein_id="CA80867.1"
/db_xref="GI:429108"
/db_xref="SWISS-PROT:P43282"
/translation="METFLTSESVNESHHPDKLCDVSDAILDACLEDDPESKAVACET
CTKTNMVMVFGELTTKATVDYERKIVRDCRGIFGSADVGLADNCKVLYVNIQOSPD
IAQGVHGLTKRKEPEIGAGDQGHMFATDEPELMLPLTHVATKLGAKLTERKNT
CPMLRPDGTQVTEYKNDNGAMVP1RVHVTILSTOHDEVTNDOJLAOLKEHVTKPV
IPAKYLDENTIFHLNPSGRFVIGPHGDALTRKIIIDTYGGMAGHAGGAFSGKDP
KVDKSGAYIVROAKSVYASGLARCTIVQSYAIGVAEPLSVFDTYKTTGTTDPKDL
VLIKENDFPRGMSINLDLRGNGRYQKTAAYGHRDPPFTMETYKVLKPKRA"
BASE COUNT      381 a      343 c      346 g      385 t
ORIGIN

```

```

Query Match      20.5%; Score 48.2; DB 8; Length 1455;
Best Local Similarity 76.6%; Pred. No. 0.001;
Matches -59; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

```

```

QY 159 caggttcatacagaccgcgcatacagccacttggccgtgacagccgacttcaactg 218
      ||||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1
DB 1093 CAGGTTCACAGAACGACTGACGCTTACGCTTGGCCGTGATGACCCGATTTCACCTG 1152
QY 219 cgaagtgtcaagcccc 235
      || ||||| ||
DB 1153 GGAAGCTGTCAAGGTCC 1169

```

```

RESULT 39
AF321001      1531 bp  mRNA  linear  PLN 26-DEC-2000
LOCUS      Sueda maritima subsp. salsa S-adenosylmethionine synthetase 2 mRNA,
DEFINITION complete cds.
ACCESSION AF321001
VERSION AF321001.1 GI:11992266
KEYWORDS
SOURCE      Sueda maritima subsp. salsa.
ORGANISM    Sueda maritima subsp. salsa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllidae; Caryophyllales; Chenopodiaceae; Sueda.
REFERENCE   1 (bases 1 to 1531)
AUTHORS    Ma, X. and Zhang, H.
TITLE      Direct Submission
JOURNAL    Submitted (12-NOV-2000) Dept. of Biology, Plant Stress Institute,
            88 East Wenhua Rd., Jinan, Shandong 250014, P.R. China
FEATURES
            source
            1..1531
            /organism="Sueda maritima subsp. salsa"
            /sub_species="salsa"
            /db_xref="taxon:126914"
            109..1296
            /codon_start=1
            /product="S-adenosylmethionine synthetase 2"
            /protein_id="AAG42490.1"
            /db_xref="GI:11992267"
            /translation="MESFLTSESVNESHHPDKLCDVSDAVIDACLAODPSKAVACET
            CTKTNMVMVFGELTTKATVDYERKIVRDCRGIFGSADVGLADNCKVLYVNIQOSPD
            IAQGVHGLTKRKEPEIGAGDQGHMFATDEPELMLPLTHVATKLGAKLTERKNT
            CPMLRPDGTQVTEYKNDNGAMVP1RVHVTILSTOHDEVTNDOJLAOLKEHVTKPV
            IPAKYLDENTIFHLNPSGRFVIGPHGDALTRKIIIDTYGGMAGHAGGAFSGKDP
            KVDKSGAYIVROAKSVYASGLARCTIVQSYAIGVAEPLSVFDTYKTTGTTDPKDL
            KIKENDFPRGMSINLDLRGNGRYQKTAAYGHRDPPFTMETYKVLKPKRA"

```

```

CDS
BASE COUNT      378 a      352 c      356 g      445 t
ORIGIN

```

```

Query Match      20.5%; Score 48.2; DB 8; Length 1531;
Best Local Similarity 76.6%; Pred. No. 0.001;
Matches 59; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

```

```

QY 159 caggttcatacagaccgcgcatacagccacttggccgtgacagccgacttcaactg 218
      ||||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1
DB 1188 CAGGTTCACAGAACGACTGACGCTTACGCTTGGCCGTGATGACCCGATTTCACCTG 1247
QY 219 cgaagtgtcaagcccc 235
      || ||||| ||
DB 1248 GGAAGCTGTCAAGGTCC 1264

```

```

RESULT 40
PHSAMI
LOCUS      PHSAMI 1565 bp  mRNA  linear  PLN 20-MAR-1996
DEFINITION P.hybrida mRNA for S-adenosylmethionine-synthetase.
ACCESSION X82214
VERSION X82214.1 GI:559505
KEYWORDS  S-adenosylmethionine synthetase; SAM1 gene.
SOURCE     Petunia x hybrida.
ORGANISM   Petunia x hybrida
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Petunia.

```

```

REFERENCE   1 (bases 1 to 1565)
AUTHORS    Iznaki, A., Shoseyov, O. and Weiss, D.
TITLE      A petunia cDNA encoding S-adenosylmethionine synthetase
JOURNAL    Plant Physiol. 108 (2), 841-842 (1995)
MEDLINE    95334508
REFERENCE   2 (bases 1 to 1565)
AUTHORS    Weiss, D.
TITLE      Direct Submission
JOURNAL    Submitted (17-OCT-1994) D. Weiss, The Hebrew University of
            Jerusalem, P.O. Box 12, Rehovot 76100, ISRAEL

```

```

FEATURES
            source
            1..1565
            /organism="Petunia x hybrida"
            /cultivar="V-26"
            /db_xref="taxon:4102"
            /russue_type="corolla"
            /clone_id="Lambda GEM-4"
            /dev_stage="flowering"
            61..1233
            /gene="sam1"
            61..1233
            /gene="sam1"
            /EC_number="2.5.1.6"
            /codon_start=1
            /product="methionine adenosyltransferase"
            /protein_id="CAA57696.1"
            /db_xref="GI:559506"
            /db_xref="SWISS-PROT:P48498"
            /translation="METFLTSESVNESHHPDKLCDVSDAVIDACLEDDPESKAVACET
            CTKTNMVMVFGELTTKATVDYERKIVRDCRGIFGSADVGLADNCKVLYVNIQOSPD
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            CPMLRPDGTQVTEYKNDNGAMVP1RVHVTILSTOHDEVTNDOJLAOLKEHVTKPV
            IPAKYLDENTIFHLNPSGRFVIGPHGDALTRKIIIDTYGGMAGHAGGAFSGKDP
            KVDKSGAYIVROAKSVYASGLARCTIVQSYAIGVAEPLSVFDTYKTTGTTDPKDL
            TLIKENDFPRGMSINLDLRGNGRYQKTAAYGHRDPPFTMETYKVLNPKRA"

```

```

CDS
BASE COUNT      418 a      350 c      355 g      442 t
ORIGIN

```

```

Query Match      20.5%; Score 48.2; DB 8; Length 1565;
Best Local Similarity 76.6%; Pred. No. 0.001;
Matches 59; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

```

```

QY 159 caggttcatacagaccgcgcatacagccacttggccgtgacagccgacttcaactg 218
      ||||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1 ||||| 1
DB 1140 CAGGTTCACAGAACGACTGACGCTTACGCTTGGCCGTGATGACCCGATTTCACCTG 1199
QY 219 cgaagtgtcaagcccc 235
      || ||||| ||
DB 1200 GGAAGCTGTCAAGGTCC 1216

```

[illegible]

	Singapore
FEATURES	Location/Qualifiers
source	. .4459 /organism="Brassica juncea" /db_xref="taxon:3707"
mRNA	<2275..>3456 /product="S-adenosylmethionine synthetase"
CDS	2275..3456 /note="MSAMS2" /codon_start=1 /product="S-adenosylmethionine synthetase" /protein_id="AGI17666.1" /db_xref="GI:10443981"
BASE COUNT	1284 a 924 c 877 g 1374 t
ORIGIN	A ^a
Query Match	20.1%; Score 47.2; DB 8; Length 4459;
Best Local Similarity	76.3%; Pred. No. 0.0022;
Matches 58; Conservative	0; Mismatches 18; Indels 0; Gaps 0;
OY 160	aggtcatcaaacgcccgcacataaggccacttggcgtgacgacgccgacctcacctgc 219
Dd 3355	ACGTTCTTGAACACTGCCTTAGGTGTCATTTGGAGAAGGACGAGCTGACTACCTGG 3414
OY 220	gaagtcggtcaagcccc 235
Dd 3415	GAGTGTTGTGAACCAC 3430
RESULT 44	
AF008568	
LOCUS	AF008568 820 bp mRNA linear PLN 02-OCT-1997
DEFINITION	Chlamydomonas reinhardtii S-adenosylmethionine synthetase (CHRSAMS)
ACCESSION	AF008568
KEYWORDS	partial cds.
SOURCE	AF008568.1 GI:2454483
ORGANISM	Chlamydomonas reinhardtii. Chlamydomonas reinhardtii. Eukaryota: Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadales; Chlamydomonas. 1 (bases 1 to 820) Kim,J.Y., Lee,K.O. and Lee,S.H. Unpublished
REFERENCE	2 (bases 1 to 820) Kim,J.Y., Lee,K.O. and Lee,S.H. Direct Submission Submitted (16-JUN-1997) Biology, Yonsei University, Sinchon-dong 134, Seodaemun-gu, Seoul 120-749, Korea
JOURNAL	Location/Qualifiers
FEATURES	1..820 /organism="Chlamydomonas reinhardtii" /strain="137C" /db_xref="taxon:3055"
source	<1..820 /gene="CHRSAMS" /name="CHRSAMS" /codon_start=1 /product="S-adenosylmethionine synthetase" /protein_id="AAB71833.1" /db_xref="GI:2454484" /translation="DIMEHIKPVPAKKYIDKTIIFHLNPSGRFVIGPHDGAGLTGR
gene	
CDS	

BASE COUNT	166 a	233 c	268 g	153 t
Query Match	20.0%; Score 47; DB 8; Length 820;			
Best Local Similarity	78.9%; Pred. No. 0.0022;			
Matches	56; Conservative	0; Mismatches	15; Indels	0; Gaps 0;
Db	161	458	221	518
LOCUS	AF346305	1572 bp	mRNA	linear
DEFINITION	Elaeagnus umbellata S-adenosyl-L-methionine synthetase (SAMS1)			
ACCESSION	AF346305	Complete cds.		
VERSION	AF346305.1	GI:13540315		
KEYWORDS	Elaeagnus umbellata.			
SOURCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Elaeagnaceae; Elaeagnus.			
REFERENCE	Lee,S.H. and An,C.S. Structures and expression patterns of two cDNA clones encoding S-adenosyl-L-methionine synthetase from the root nodule of Elaeagnus umbellata			
AUTHORS	Unpublished			
TITLE	2 (bases 1 to 1572)			
JOURNAL	Lee,S.H. and An,C.S. Direct Submission			
AUTHORS	Submitted (06-FEB-2001) School of Biological Sciences, Seoul National University, Seoul 151-742, Korea			
TITLE	Location/Qualifiers			
JOURNAL	1. 1572			
AUTHORS	/organism="Elaeagnus umbellata"			
TITLE	/db_xref="taxon:43233"			
JOURNAL	/tissue_type="root nodule"			
AUTHORS	1. 1572			
TITLE	/gene="SAMS1"			
JOURNAL	83. 1264			
AUTHORS	/EC_number="2.5.1.6"			
TITLE	/codon_start=1			
JOURNAL	/product="S-adenosyl-L-methionine synthetase"			
AUTHORS	/protein_id="AAK29409.1"			
TITLE	/db_xref="GI:13540316"			
JOURNAL	/translation="METFLETSSEVNEGHPDKLQDISAVIADACLAQDPDSKVACETCSKINVMVFGELITKANVDYERIVRPTCAIIFVSDVDLADNCKVLVINIQOSPDIAGVGHGFTKRPBELTACGQGHFAGYATDETPBYMLSHVLTATKIGARLTVRKNGTCPMLRPDGKTQVIVVEYENENGAMVPVWVVLSTOHDEVTVDDEIAADLKEHVIRPVIPKYLIDERTILFHLNPSGRVIGGPHQDAGLTGRTKITIPYGGWGAHGGAPEGKRPTKYDRSGKVIYRQAKSLVANGLARRCILVOYSVYAIQVPEPLSVFSDYTGIGQIPDKELI NIKENEDFERGMITTINLDLRGNGEFLKLTAGYGHGRDDPDFTWEIVKPKWERPQ S"			
BASE COUNT	425 a	333 c	369 g	445 t
ORIGIN				
Query Match	19.8%; Score 46.6; DB 8; Length 1572;			
Best Local Similarity	75.3%; Pred. No. 0.0031;			
Matches	58; Conservative	0; Mismatches	19; Indels	0; Gaps 0;

Tue Aug 20 07:55:44 2002

us-09-198-779b-1.rge

Page 25

QY	159	caagttcatcaagaacgcgcgcacatacggccactttggcgtgcgcgcgcgaactcaactg	218
Db	1162	CAGGTCCTCTTAAGACACGACGAGGTATGGACACTTTGGAAAGATGACCCAGACTTCACATG	1221
QY	219	cgagggtgtcaagcccc	235
Db	1222	GGAGATTGTGAAGCCCC	1238

Search completed: August 20, 2002, 01:29:07
Job time: 7896 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 23:16:15 ; Search time 1800.16 Seconds
(without alignments)
1761.946 Million cell updates/sec

Title: US-09-198-779b-1

Perfect score: 235
Sequence: 1 gtttcgctagcctcgtg.....ctgcgaggtgttcaagccccc 235

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estrov:*
6: em_estrpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_hiv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	122	51.9	232	10	BM340942
2	122	51.9	512	10	BM075638
3	122	51.9	555	10	BM267205
4	122	51.9	594	10	BM334082
5	122	51.9	650	10	BM339093
6	122	51.9	746	10	BM267021
7	121	51.5	528	9	AI948255
8	121	51.5	554	9	AI795380
9	121	51.5	554	9	AM000206
10	121	51.5	583	9	AM067167
11	121	51.5	605	9	AI855043
12	121	51.5	626	10	BM078637
13	121	51.5	670	10	BM074388
14	120.4	51.2	513	10	BM332958
15	120.4	51.2	609	10	BM347524
16	120.4	51.2	645	10	BM339768
17	120.4	51.2	745	10	BM268790

C 18	119	50.6	548	10	BM348643	BM348643	MEST294-C
C 19	117	49.8	595	9	AI691859	AI691859	606011C12
C 20	110	46.8	752	10	BM336997	BM336997	MEST201-H
C 21	107.6	45.8	637	10	BM079570	BM079570	MEST196-D1
C 22	107.4	45.7	492	9	AM497500	AM497500	660052H09
C 23	103.8	44.2	530	10	BM079887	BM079887	MEST101-A
C 24	100.4	42.7	435	10	BM336874	BM336874	MEST200-A
C 25	100	42.6	533	10	BM336766	BM336766	MEST198-F
C 26	100	42.6	627	9	AI861345	AI861345	614012F08
C 27	100	42.6	648	10	BM350900	BM350900	MEST170-D
C 28	98	41.7	409	9	AI901593	AI901593	618007E09
C 29	85	36.2	581	9	AI714565	AI714565	605059E11
C 30	82	34.9	411	9	AI978238	AI978238	614042B09
C 31	76.8	32.7	499	10	BG550027	BG550027	947080E01
C 32	76.8	32.7	502	10	BG549665	BG549665	947080E01
C 33	76.8	32.7	503	10	BG549664	BG549664	947080E01
C 34	76.2	32.4	602	9	AI657373	AI657373	486093H12
C 35	75.6	32.2	413	10	BI388940	BI388940	949047F08
C 36	75.6	32.2	463	9	AI738382	AI738382	606049C06
C 37	75.6	32.2	490	10	BG550028	BG550028	947080E01
C 38	75.6	32.2	504	10	BE511080	BE511080	946057F06
C 39	75.6	32.2	554	9	AI737785	AI737785	606041C09
C 40	75.6	32.2	581	9	AI734421	AI734421	606031B05
C 41	75.6	32.2	588	9	AI734316	AI734316	606029E07
C 42	75.6	32.2	589	9	AI737411	AI737411	606040B05
C 43	75.6	32.2	591	10	BE511079	BE511079	946057F06
C 44	75.6	32.2	632	9	AM062087	AM062087	660009F01
C 45	75.4	32.1	414	9	AI920328	AI920328	603019C04

ALIGNMENTS

RESULT 1
BM340942/c 232 bp mRNA linear EST 16-JAN-2002
LOCUS MEST328-A09.T3 ISGM5-RN Zea mays cDNA clone MEST328-A09 3', mRNA
DEFINITION
ACCESSION BM340942
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BM340942
MEST328-A09.T3 ISGM5-RN Zea mays cDNA clone MEST328-A09 3', mRNA
sequence.
BM340942
BM340942.1 GI:181711102
EST.
Zea mays.
Zea mays.
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 232)
Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S.
Expressed Sequence Tags from B73 Maize: various stages and tissues
including seedlings treated with a variety of hormones
Unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
6405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
Individual basecall and confidence value were assigned using the
Phred software,
(<http://depts.washington.edu/ventures/collabtr/direct/index.htm#b>
rt). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/softlab/lucy/>).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the
poly-T and the high-quality region were replaced with N's to serve
as spacers.
PCR Primers
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers

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source
1. .232
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST328-A09"
/clone_lib="ISUM5-RN"
/tissue_type="mixed"
/lab_host="DH10B"
/notes="Vector: pT73PAC; Site_1: EcoRI; Site_2: NotI;
tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
mixed mature tissues (17, 21, 38, 69, 77 DAG), kernels
(3, 5, 10, 15, 20, 25, 30, DAP), Adventitious roots (65 DAG
), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0
cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated
first ear, ear shank, etiolated seedlings, callus,
cycloheximide-treated callus, Anaerobic treated seedlings
, NAA (a-Naphthalene acetic acid)-treated seedlings,
kinetin-treated seedlings, ACPG
(1-aminocyclopropane-1-carboxylic acid)-treated seedlings,
Brassinolide-treated seedlings, ABA (abscisic acid
)-treated seedlings, GA (Gibberellic acid)-treated
seedlings, JA (Jasmonic acid)-treated seedlings. ds-cDNA
molecules were generated as follows. First-strand cDNA was
prepared from oligo-dT selected mRNA by priming with a
NotI oligo-dT primer (5'
ACTGGAAGAATTCGCGCCGACGAAATTTTTTTTTTTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA PolI-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT73PAC vector. The library
then went through one round of normalization to COT value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996)."

BASE COUNT      72 a      52 c      45 g      63 t
ORIGIN

Query Match      51.9%; Score 122; DB 10; Length 232;
Best Local Similarity 76.7%; Pred. No. 1.1e-24;
Matches 122; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 1 gtcttcgctagctcgtgtagacagatcgacgtcgcacatctgataatgacggtcc 60
Db 217 GTTTCCGCTAGCGCTCGGTGACAGATCGACGCTGCCATGCTAATAATGACGGTCC 158
Qy 61 tgatccattgttcgtgtgtatataatgttataatgagcagacaacacgtacgt 120
Db 157 TGATCCATGTTCCGTTGTTGTTATTAATGTTGATTAATGAGCAGACACACGCTACGT 98
Qy 121 tnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 159
Db 97 TACTCTCTGTCTGTCTGTCTGTTCATGATGCTCTC 59

RESULT 2
BM075638/c 512 bp mRNA linear EST 13-NOV-2001
LOCUS MEST358-C04.T3 ISUM5-RN Zea mays cDNA clone MEST358-C04 3', mRNA
DEFINITION sequence.
ACCESSION BM075638
VERSION BM075638
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 512)
AUTHORS Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S.
TITLE Expressed Sequence Tags from B73 Maize: various stages and tissues
including seedlings treated with a variety of hormones

```

```

JOURNAL
COMMENT
Unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
4405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
Individual basecall and confidence value were assigned using the
phred software.
(<http://depts.washington.edu/ventures/collablt/direct/index.htm>#b
rt). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/soflab/>).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the
poly-T and the high-quality region were replaced with N's to serve
as spacers.
PCR Primers
FORWARD: Forward PCR primer sequence, primer T7-1 (AA TAC GAC TCA
CTA TAC)
BACKWARD: Backward PCR primer sequence, primer T3 (ATT AAC CCT CAC
TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
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/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST358-C04"
/clone_lib="ISUM5-RN"
/tissue_type="mixed"
/lab_host="DH10B"
/notes="Vector: pT73PAC; Site_1: EcoRI; Site_2: NotI;
tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
mixed mature tissues (17, 21, 38, 69, 77 DAG), kernels
(3, 5, 10, 15, 20, 25, 30, DAP), Adventitious roots (65 DAG
), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0
cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated
first ear, ear shank, etiolated seedlings, callus,
cycloheximide-treated callus, Anaerobic treated seedlings
, NAA (a-Naphthalene acetic acid)-treated seedlings,
kinetin-treated seedlings, ACPG
(1-aminocyclopropane-1-carboxylic acid)-treated seedlings,
Brassinolide-treated seedlings, ABA (abscisic acid
)-treated seedlings, GA (Gibberellic acid)-treated
seedlings, JA (Jasmonic acid)-treated seedlings. ds-cDNA
molecules were generated as follows. First-strand cDNA was
prepared from oligo-dT selected mRNA by priming with a
NotI oligo-dT primer (5'
ACTGGAAGAATTCGCGCCGACGAAATTTTTTTTTTTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA PolI-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT73PAC vector. The library
then went through one round of normalization to COT value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996)."

BASE COUNT      145 a      123 c      110 g      134 t
ORIGIN

Query Match      51.9%; Score 122; DB 10; Length 512;
Best Local Similarity 76.7%; Pred. No. 1.4e-24;
Matches 122; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

Qy 1 gtcttcgctagctcgtgtagacagatcgacgtcgcacatctgataatgacggtcc 60
Db 215 GTTTCCGCTAGCGCTCGGTGACAGATCGACGCTGCCATGCTAATAATGACGGTCC 156
Qy 61 tgatccattgttcgtgtgtatataatgttataatgagcagacaacacgtacgt 120

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Db	QY	121	159	RESULT	3
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LOCUS	LOCUS	LOCUS	LOCUS	LOCUS	LOCUS
DEFINITION	DEFINITION	DEFINITION	DEFINITION	DEFINITION	DEFINITION
ACCESSION	ACCESSION	ACCESSION	ACCESSION	ACCESSION	ACCESSION
VERSION	VERSION	VERSION	VERSION	VERSION	VERSION
KEYWORDS	KEYWORDS	KEYWORDS	KEYWORDS	KEYWORDS	KEYWORDS
SOURCE	SOURCE	SOURCE	SOURCE	SOURCE	SOURCE
ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM	ORGANISM
REFERENCE	REFERENCE	REFERENCE	REFERENCE	REFERENCE	REFERENCE
AUTHORS	AUTHORS	AUTHORS	AUTHORS	AUTHORS	AUTHORS
TITLE	TITLE	TITLE	TITLE	TITLE	TITLE
JOURNAL	JOURNAL	JOURNAL	JOURNAL	JOURNAL	JOURNAL
COMMENT	COMMENT	COMMENT	COMMENT	COMMENT	COMMENT

Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schmale@iastate.edu

Individual Basecall and confidence value were assigned using the
phred software,
([#http://depts.washington.edu/ventures/collabtr/direct/index.htm](http://depts.washington.edu/ventures/collabtr/direct/index.htm);
rt). Overall sequence quality assessment and vector trimming were
conducted using the lincy software (<http://www.tlgr.org/sofflab/>)
Lincy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the
poly-T and the high-quality region were replaced with N's to serve
as spacers.

PCR primers
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

Location/Qualifiers
1..555

/organism="Zea mays"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /clone="MEST31-001"
 /clone_1lp="150M-RN"
 /tissue_type="mixed"
 /lab_host="DH10B"
 /note="vector: pT73p3AC; Site_1: EcoRI; Site_2: NotI;
 Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
 mixed mature tissues (17, 21, 38, 69, 77 DAG), kernels
 (3, 5, 10, 15, 20, 25, 30, DAG), Adventitious roots (65 DAG),
 3, Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0
 cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated
 first ear, ear shank, etiolated seedlings, callus,
 Cycloheximide-treated callus, Anaerobic treated seedlings
 NMA (α-Naphthalene acetic acid)-treated seedlings,
 kinetin-treated seedlings, ACPc
 1-aminocyclopropane-1-carboxylic acid)-treated seedlings,
 Brassinolide-treated seedlings, ABA (Abscissic acid
 -treated seedlings), GA (Gibberellic acid)-treated
 seedlings, JA (Jasmonic acid)-treated seedlings, ds-cDNA
 molecules were generated as follows. First-strand cDNA was
 prepared from oligo-dT selected mRNA by priming with a
 NotI oligo-dT primer (5'

AACGCGAAGATTTCGCGCCGACGAGATTTTTTTTTTTTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA polymerase-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT7T3PAC vector. The library then went through one round of normalization to Cot value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."

Query Match	Similarity	Score	DB	Length
Best Local	76.7%	Pred. No. 1,4e+24		555;
Matches	122: Conservative	0; Mismatches	37; Indels	0; Gaps
Qy	1	gttttcgclctagcgcggtgagacagatcgacgcgtcccatgctgataataatgagcgtcc	60	
Db	217	gTTTTCCGTCGTAGCCTCGGTGGAGATCGACGCTGCCCATCTGATTAATGAGCGTCC	158	
Qy	61	tgatccaatgttcgctgtgtgttataatgttcataatggacgagacacaaacgttaagt	120	
Db	157	TGATCCAAATGTCGCTTGTTGTTATATGTTGATATGAGCAGACACAAACGCTACGT	98	
Qy	121	TT	159	
Db	97	TACTCTCTGTCTGTCTGTCTGTCTGTTTCCATGACGCAATTGTCTC	59	

RESULT	4
BM334082/c	
LOCUS	
DEFINITION	BM334082 594 bp mRNA linear EST 16-JAN-2002 MEST132-C11.T3 ISUMS-RN Zea mays CDNA clone MEST132-C11 3', mRNA
ACCESSION	Sequence. BM334082
VERSION	BM334082.1 GI:18164243
KEYWORDS	EST.
SOURCE	Zea mays.
ORGANISM	Zea mays. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 594) Went,J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S. Expressed Sequence Tags from B73 Maize: various strages and tissues including seedlings treated with a variety of hormones unpublished (2001) Contact: Patrick S. Schnable
JOURNAL	
COMMENT	

G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel.: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
Individual basical and confidence value were assigned using the
phred software,
<<http://deps.washington.edu/ventures/colabtr/direct/index.htm#html>>
rt). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<<http://www.tigr.org/software/>>).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the
poly-T and the high-quality region were replaced with N's to serve
as spacers.
PCR Primers
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
1..594
/organism="Zea mays"

Schnable Laboratory
Iowa State University
GA05 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu
Individual basecall and confidence value were assigned using the
phred software,
(<http://depts.washington.edu/ventures/collabutr/direct/index.htm#>
tr). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/softlab/lucy/>).
Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the
poly-T and the high-quality region were replaced with N's to serve
as spacers.
PCR Primers
FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)
BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).
Location/Qualifiers
1. .650
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="MEST336-F10"
/clone_1lb="ISUM5-RN"
/tissue="mixed"
/lab_host="DH10B"
/note="Vector: pT73PAC; Site_1: EcoRI; Site_2: NotI;
Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
Mixed mature tissues (17, 21, 38, 69, 77 DAG), kernels
(3, 5, 10, 15, 20, 25, 30, DAP), Adventitious roots (65 DAG
) , Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0
DAP)

Cyclonhexamide-treated callus, Anaerobic treated seedlings
NAA (α-Naphthalene acetic acid)-treated seedlings,
Kinetin-treated seedlings, ACR

biass-molecule-treated seedlings, ABA (Abscisic acid)-treated seedlings, GA (Gibberellic acid)-treated seedlings, JA (Jasmonic acid)-treated seedlings. ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5'-AAGTCAGACATTCGCGCCGACGAGATTTTTTTTTTTTTT-3'). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the

[illegible]

Db	95	TACTCTCGTCTGTCGTGTGTTGCATGCATTTGTC	57
RESULT	6		
LOCUS	BM267021/c	746 bp	linear
DEFINITION	BM267021	EST 18-DEC-2001	
ACCESSION	BM267021		
VERSION	BM267021.1	GI:17930061	
KEYWORDS	EST.		
SOURCE	Zea mays.		
ORGANISM	Zea mays.		
REFERENCE	Phakaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogonae; Zea.		
AUTHORS	1 (bases 1 to 746)		
TITLE	Men,T.J., Qiu,F., Guo,L., Ashlock,D.A and Schnable,P.S.		
JOURNAL	Expressed Sequence Tags from B73 Maize: various stages and tissues including seedlings treated with a variety of hormones		
COMMENT	Unpublished (2001) Contact: Patrick S. Schnable Schnable Laboratory Iowa State University 6405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA Tel: 515-294-0975 Fax: 515-294-2299 Email: schnable@iastate.edu Individual basical and confidence value were assigned using the phned software, (http://depts.washington.edu/ventures/collabtr/direct/index.htm#btr). Overall sequence quality assessment and vector trimming were conducted using the Lucy software (http://www.tigr.org/softlab/lucy/). Lucy parameters were set to ensure an overall trimmed quality of 97.5% or better without any vector fragments in the chosen high-quality region of each sequence. Low-quality bases between the poly-T and the high-quality region were replaced with N's to serve as spacers. PCR Primers FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG) BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG) Seq primer: primer T3 (ATT AAC CCT CAC TAA AG). Location/Qualifiers 1. 746 /organism="Zea mays" /cultivar="B73" /db_xref="taxon:4577" /clone="MEST389-B08" /clone_id="ISUM5-RN" /tissue_type="mixed" /lab_host="DH108" /note="Vector: pT73PAC; Site_1: EcoRI; Site_2: NotI; Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG), Mixed mature tissues (17, 21, 38, 69, 77 DAG), kernels (3, 5, 10, 15, 20, 25, 30, DAP), Adventitious roots (65 DAG), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.0 cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated first ear, ear shank, etiolated seedlings, callus, Cycloheximide-treated callus, Anaerobic treated seedlings, NAA (a-Naphthalene acetic acid)-treated seedlings, Kinetin-treated seedlings, ACP (1-aminocyclopropane-1-carboxylic acid)-treated seedlings, Brassinolide-treated seedlings, ABA (Abscisic acid)-treated seedlings, GA (Gibberellic acid)-treated seedlings, JA (Jasmonic acid)-treated seedlings, ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5', AATCGAAGAATTCGCGCGCAGCAATTTTTTTTTTTTTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA Pol-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the		

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ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pTRT3PAC vector. The library
then went through one round of normalization to Cot value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996)."
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BASE COUNT	202 a	183 c	168 g	193 t
ORIGIN				
Query Match	51.9%; Score 122; DB 10; Length 746;			
Best Local Similarity	76.7%; Pred. No. 1.6e-24;			
Matches 122; Conservative	0; Mismatches 37; Indels 0; Gaps 0;			
OY	1 gtcttcgcctaagcctcgtagacagatcgaacctgccaagtctataaatgacggtcc 60 Db 215 GTTTCCCTGATAGCCTCGTCGGTAGACAGATCGACGTGCCCATGCTGTAATAATGGACGGTC 156 OY 61 tgattccattgttcgttggtgttataatgattgtatatattgagcaaggacaacagtaagt 120 Db 155 TGATCCATTGGTGCTGTGGTTATTATATGTTGTATTAATGTGACACAGCACACACTACGT 96 OY 121 tnn 159 Db 95 TACTCTCTGTCTGTCTGTGTGTTGCATGGCACTTGTCTC 57 			
RESULT 7	A1948255 528 bp mRNA linear EST 19-AUG-1999			
A1948255/c	LOCUS			
DEFINITION	603038C05.x1 603 - stressed root cDNA library from Wang/Bohnert lab			
ACCESSION	Zea mays cDNA, mRNA sequence.			
VERSION	A1948255			
KEYWORDS	A1948255.1 GI:5740565			
SOURCE	EST.			
ORGANISM	Zea mays.			
JOURNAL	Unpublished (1999)			
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 603039 row: C column: 05. Location/Qualifiers 1..528 /organism="Zea mays" /cultivar="B73" /db_xref="taxon:4577" /clone_lib="603 - stressed root cDNA library from Wang/Bohnert lab" /tissue_type="seedling" /dev_stage="salt stress" /lab_host="E. coli XL Gold" /note="Organ: root; Vector: pBluescriptII SK(+) XR; Seedling stressed root cDNA library from Wang/Bohnert lab"			
REFERENCE	Maize ESTs from various cDNA libraries sequenced at Stanford University			
AUTHORS	Walbot, V			
TITLE	Maize ESTs from various cDNA libraries sequenced at Stanford University			
FEATURES	Source			
BASE COUNT	147 a 127 c 126 g 127 t 1 others			
ORIGIN				
Query Match	51.5%; Score 121; DB 9; Length 528;			
Best Local Similarity	100.0%; Pred. No. 2.7e-24;			
Matches 121; Conservative	0; Mismatches 0; Indels 0; Gaps 0;			

QY 1 gtttcgctacgctcgtgagacagatcgacgctgccatgctgataatgagcgtcc 60
|||||
Db 124 GTTTCCGCTACCGCTCGGAGACATCACCCTGCTGATTAATGGAGCGTCC 65
|||||
QY 61 tgatccatgttcgtgtgtatataatgtgtatattgagcagagacacacgtaagt 120
|||||
Db 64 TGATCCATGTTGCTGTGTATTAAATGTTATTAATTGAGCAGACACACAGTACGT 5
|||||
QY 121 t 121
|
Db 4 T 4
|
RESULT 8
AI795380 554 bp mRNA linear EST 02-JUL-1999
LOCUS 614009A12.x2 614 - root cDNA library from Walbot Lab Zea mays cDNA,
DEFINITION mRNA sequence.
ACCESSION AI795380
VERSION AI795380.1 GI:5343195
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
REFERENCE 1 (bases 1 to 554)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL University
COMMENT Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 614009 row: A column: 12.
Location/Qualifiers
1..554
/organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="614 - root cDNA library from Walbot Lab"
/tissue_type="root"
/dev_stage="3-4 days old"
/lab_host="XLDLR"
/note="Organ: root; Vector: pBluescriptII SK+; Site_1:
EcORI; Site_2: XhoI; 3-4 days old root tissue from Walbot
Lab (LM)"
BASE COUNT 149 a 128 c 128 g 149 t
ORIGIN
Query Match 51.5%; Score 121; DB 9; Length 554;
Best Local Similarity 100.0%; Pred. No. 2,8e-24;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AM000206 554 bp mRNA linear EST 08-SEP-1999
LOCUS 614009A12.Y1 614 - root cDNA library from Walbot Lab Zea mays cDNA,
DEFINITION mRNA sequence.
ACCESSION AM000206
VERSION AM000206.1 GI:5847127
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
REFERENCE 1 (bases 1 to 554)
AUTHORS Walbot,V.
TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
JOURNAL University
COMMENT Unpublished (1999)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Plate: 614009 row: A column: 12.
Location/Qualifiers
1..554
/organism="Zea mays"
/cultivar="W23"
/db_xref="taxon:4577"
/clone_lib="614 - root cDNA library from Walbot Lab"
/tissue_type="root"
/dev_stage="3-4 days old"
/lab_host="XLDLR"
/note="Organ: root; Vector: pBluescriptII SK+; Site_1:
EcORI; Site_2: XhoI; 3-4 days old root tissue from Walbot
Lab (LM)"
BASE COUNT 149 a 128 c 128 g 149 t
ORIGIN
Query Match 51.5%; Score 121; DB 9; Length 554;
Best Local Similarity 100.0%; Pred. No. 2,8e-24;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtttcgctacgctcgtgagacagatcgacgctgccatgctgataatgagcgtcc 60
|||||
Db 416 GTTTCCGCTACCGCTCGGAGACATCACCCTGCTGATTAATGGAGCGTCC 475
|||||
QY 61 tgatccatgttcgtgtgtatataatgtgtatattgagcagagacacacgtaagt 120
|||||
Db 476 TGATCCATGTTGCTGTGTATTAAATGTTATTAATTGAGCAGACACACAGTACGT 535
|||||
QY 121 t 121
|
Db 536 T 536
|
RESULT 10
AM067167 583 bp mRNA linear EST 12-OCT-1999
LOCUS 683016F05.x1 683 - 14 day immature embryo from Hake lab (HS) Zea
DEFINITION mays cDNA, mRNA sequence.
ACCESSION AM067167
VERSION AM067167.1 GI:6022239
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
REFERENCE 1 (bases 1 to 583)
AUTHORS Walbot,V.

TITLE Maize ESTs from various cDNA libraries sequenced at Stanford University
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 683016 row: F column: 05.
 Location/Qualifiers
 1. 583
 /organism="Zea mays"
 /cultivar="B73"
 /db_xref="taxon:4577"
 /clone_lib="683 - 14 day immature embryo from Hake lab (HS)"
 /tissue_type="embryo"
 /dev_stage="14 days after pollination"
 /lab_host="DH10B"
 /note="Organ: embryo; Vector: pBKCMV (Stratagene's Zap Express); Site_1: XhoI; Site_2: EcoRI; Directionally cloned, 14 day immature embryo library created with Stratagene's Zap Express cDNA protocol."
 BASE COUNT 155 a 135 c 131 g 162 t
 ORIGIN

Query Match 51.5%; Score 121; DB 9; Length 583;
 Best Local Similarity 100.0%; Pred. No. 2.8e-24;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtcttcgctagcgtcggtgagacagatcgacgctgcccacgtcgataatagacgctcc 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 145 GTTTCGCTAGCCTCGGTGACGATCGACGCTGCCCATGCTGATTAATGAGACGGTCC 86
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 tgaaccattgtctgtgtatcaatgtgtataatgacagacacacacgtact 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 85 TGATCCATTGTTGCTGTGTTATTATGTTGTTATTAATTGACGACGACACGACTACT 26
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 t 121
 |
 DB 25 T 25

RESULT 11
 A1855043/c 605 bp mRNA linear EST 02-FEB-2000
 LOCUS 606074C08.x1 606 - Ear tissue cDNA library from Schmidt lab Zea
 DEFINITION mays cDNA, mRNA sequence.
 ACCESSION A1855043
 VERSION A1855043.1 GI:5499176
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 605)
 Walbot,V.
 Maize ESTs from various cDNA libraries sequenced at Stanford University
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 606074 row: C column: 08.
 Location/Qualifiers

source 1. 605
 /organism="Zea mays"
 /cultivar="Ohio43"
 /db_xref="taxon:4577"
 /clone_lib="606 - Ear tissue cDNA library from Schmidt lab"
 /tissue_type="mixed"
 /dev_stage="ear length from 0.5 cm - 2.0 cm"
 /lab_host="XLDOR (Stratagene)"
 /note="Organ: Immature ear; Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; Mixed ear tissue cDNA library from Schmidt lab"
 BASE COUNT 161 a 145 c 136 g 163 t
 ORIGIN

Query Match 51.5%; Score 121; DB 9; Length 605;
 Best Local Similarity 100.0%; Pred. No. 2.8e-24;
 Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtcttcgctagcgtcggtgagacagatcgacgctgcccacgtcgataatagacgctcc 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 145 GTTTCGCTAGCCTCGGTGACGATCGACGCTGCCCATGCTGATTAATGAGACGGTCC 86
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 tgaaccattgtctgtgtatcaatgtgtataatgacagacacacacgtact 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 85 TGATCCATTGTTGCTGTGTTATTATGTTGTTATTAATTGACGACGACACGACTACT 26
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 t 121
 |
 DB 25 T 25

RESULT 12
 BM078637/c 626 bp mRNA linear EST 14-NOV-2001
 LOCUS MEST122-D04.T3 ISDN4-TN Zea mays cDNA clone MEST122-D04 3', mRNA
 DEFINITION sequence.
 ACCESSION BM078637
 VERSION BM078637.1 GI:16925569
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 626)
 Qiu,F., Cui,F., Guo,L., Ashlock,D.A., Wen,T.J. and Schnable,P.S.
 Expressed Sequence Tags from B73 Maize Seedlings and Silks
 Unpublished (2001)
 Contact: Patrick S. Schnable
 Schnable Laboratory
 Iowa State University
 G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
 Tel: 515-294-0975
 Fax: 515-294-2299
 Email: schnable@iastate.edu
 Individual basecall and confidence value were assigned using the
 phred software,
 (<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#b
 rt). Overall sequence quality assessment and vector trimming were
 conducted using the lacy software (<http://www.tigr.org/softlab/>).
 Lacy parameters were set to ensure an overall trimmed quality of
 97.5% or better without any vector fragments in the chosen
 high-quality region of each sequence. Low-quality bases between the
 poly-T and the high-quality region were replaced with N's to serve
 as spacers.
 PCR primers
 FORWARD: Forward PCR primer sequence, primer T7-1 (AA TAC GAC TCA
 CTA TAG)
 BACKWARD: Backward PCR primer sequence, primer T3 (ATT AAC CCT CAC
 TAA AG)
 Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

FEATURES source

Location/Qualifiers
1. 626
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone_lib="ISUM4-TN"
/issue_type="Seedling and silk"
/lab_host="DH10B"
/note="Vector: pT73PAC; Site_1: EcoRI; Site_2: NotI; ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5', AACTGAGAGATTCCGCCGCGAGATTTTCTTTTCTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT73PAC vector. The library then went through one round of normalization to Cot value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."

BASE COUNT 164 a 149 c 145 g 168 t
ORIGIN

Query Match 51.5%; Score 121; DB 10; Length 626;
Best Local Similarity 100.0%; Pred. No. 2.9e-24;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtttcgctagcctcgctgacacagatcgacgtcccatgctgataatgacgcttc 60
|||||
DB 145 GTTTCCGCTAGCCTCGGTGGACAGATCGACCTCCCATGCTGTAATAGACGCTCC 86
|||||
OY 61 tgatccattgttcgtgtgtatgataatgtgataatgacagacacacgctgact 120
|||||
DB 85 TGATCCATTGTTGTTGTGTATTATGTTATATTGATGACGACGACACACGCTAGCT 26
|||||
OY 121 t 121
|
DB 25 T 25

RESULT 13
BM074388/c 670 bp mRNA linear EST 13-NOV-2001
LOCUS MEST185-E10.T3 ISUM4-TN Zea mays cDNA clone MEST185-E10 3', mRNA
DEFINITION sequence.
ACCESSION BM074388
VERSION BM074388.1 GI:16919855
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 670)
Olu,F., Cul,F., Guo,L., Ashlock,D.A., Wen,T.J. and Schnable,P.S.
Expressed Sequence Tags from B73 Maize Seedlings and Silks
Unpublished (2001)
Contact: Patrick S. Schnable
Schnable Laboratory
Iowa State University
6405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299
Email: schnable@iastate.edu

Individual basacall and confidence value were assigned using the
phred software,
(<http://depts.washington.edu/ventures/collabtr/direct/index.htm#b>
rt). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/softlab/>).

Lucy parameters were set to ensure an overall trimmed quality of
97.5% or better without any vector fragments in the chosen
high-quality region of each sequence. Low-quality bases between the
poly-T and the high-quality region were replaced with N's to serve
as spacers.
PCR Primers
FORWARD: Forward PCR primer sequence, primer T7-1 (AA TAC GAC TCA
CTA TAG)
BACKWARD: Backward PCR primer sequence, primer T3 (ATT AAC CCT CAC
TAA AG)
Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

FEATURES source

Location/Qualifiers
1. 670
/organism="Zea mays"
/cultivar="B73"
/db_xref="taxon:4577"
/clone_lib="MEST185-E10"
/clone_lib="ISUM4-TN"
/issue_type="Seedling and silk"
/lab_host="DH10B"
/note="Vector: pT73PAC; Site_1: EcoRI; Site_2: NotI; ds-cDNA molecules were generated as follows. First-strand cDNA was prepared from oligo-dT selected mRNA by priming with a NotI oligo-dT primer (5', AACTGAGAGATTCCGCCGCGAGATTTTCTTTTCTTTT). The resulting DNA:RNA hybrid was treated with RNase H and used as a template for DNA PolI-catalyzed second strand synthesis. After the addition of EcoRI adaptors, the ds-cDNAs were digested with NotI and size-selected. The resulting molecules were directionally cloned into the EcoRI and NotI sites of the pT73PAC vector. The library then went through one round of normalization to Cot value of 5 based on the methods of Marcelo Bento Soares (Genome Research 6: 791-806, 1996)."

BASE COUNT 173 a 158 c 150 g 178 t 11 others
ORIGIN

Query Match 51.5%; Score 121; DB 10; Length 670;
Best Local Similarity 100.0%; Pred. No. 2.9e-24;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 gtttcgctagcctcgctgacacagatcgacgtcccatgctgataatgacgcttc 60
|||||
DB 151 GTTTCCGCTAGCCTCGGTGGACAGATCGACCTCCCATGCTGTAATAGACGCTCC 92
|||||
OY 61 tgatccattgttcgtgtgtatgataatgtgataatgacagacacacgctgact 120
|||||
DB 91 TGATCCATTGTTGTTGTGTATTATGTTATATTGATGACGACGACACACGCTAGCT 32
|||||
OY 121 t 121
|
DB 31 T 31

RESULT 14
BM332958/c 513 bp mRNA linear EST 16-JAN-2002
LOCUS MEST182-A04.T3 ISUM5-RN Zea mays cDNA clone MEST182-A04 3', mRNA
DEFINITION sequence.
ACCESSION BM332958
VERSION BM332958.1 GI:18163119
KEYWORDS EST.
SOURCE Zea mays.
ORGANISM Zea mays.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 513)
Wen,T.J., Olu,F., Guo,L., Ashlock,D.A. and Schnable,P.S.
Expressed Sequence Tags from B73 Maize: various stages and tissues
including seedlings treated with a variety of hormones
Unpublished (2001)

Individual basacall and confidence value were assigned using the
phred software,
(<http://depts.washington.edu/ventures/collabtr/direct/index.htm#b>
rt). Overall sequence quality assessment and vector trimming were
conducted using the Lucy software (<http://www.tigr.org/softlab/>).

BASE COUNT	173 a	144 c	138 g	154 t
ORIGIN				

51.28;	Score 120.4;	DB 10;	Length 609;
76.18;	Pred. No. 4.2e-24;		
0;	Mismatches 38;	Indels 0;	

agcctcgtgtagacagatcgacgcctgccatgctgataatagtgacggtcc
tagcatcggtagacagatcgacgcctgccatgctgataatagtgacggtcc

ctcgctgtgtaattaatgtgtataattgagcagacacaacacgtacgt 120
ttcgttggtattaatgtgtataattgagcagacacacacgtacgt 95

[illegible]

	645 bp	mRNA	linear	EST 16-JAN-2002
T3				
TSM5-RN				
Zea mays				
cDNA clone				
U98317-013				
27				
GenBank				

1 GI:18169928

Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
hyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PAC
nicoidae; Andropogoneae; Zea.

Qian, F., Guo, U., Ashlock, D. A. and Schnable, P. S. Sequence Tags from B73 maize: various stages and seedlings treated with a variety of hormones (2001).

nomy, Iowa State University, Ames, IA 50011-1010, USA
294-0975
294-2299

despts.washington.edu/ventures/collab/tc/direct/index.htm#>malbec@astate.edu
l bascall and confidence value were assigned using the
ware,
the high-quality region were replaced with N's to serve

primer T7-1 (AA TAC GAC TCA CTA TAG)
primer T3 (ATT AAC CCT CAC TAA AG)
primer T3 (ATT AAC CCT CAC TAA AG)

```
Location/Qualifiers
1. 645
//organism="Zea mays"
//cultivar="B73"
//db_xref="taxon:4577"
/clone="MEST312-C12"
```

```

/clone_lib="ISUM5-RN"
/tissue_type="mixed"
/lab_host="DH10B"

/notes=Vector: pTV3PAC; Site.1: EcoRI; Site.2: NotI;
Tissues: Germinated seed and seedlings (1, 2, 8, 11 DAG),
Mixed mature tissues (17, 21, 38, 69, 77 DAG), kernels
(3, 5, 10, 15, 20, 25, 30, DAP), Adventitious roots (65 DAP)
7), Tassel (3-39 cm, 53 and 56 DAG), Immature ear (0.2-3.3
cm, 53, 56, 59 DAG), Husk (73 DAG), Silk, unpollinated
first ear, ear shank, etiolated seedlings, callus,
Cyclotaxamide-treated callus, Anaerobic treated seedlings,
NMA (a Naphthalene acetic acid)-treated seedlings,
Kinetin-treated seedlings, ACPc
(1-aminocyclopropane-1-carboxylic acid)-treated seedlings,
Brassinolide-treated seedlings, ABA (abscisic acid)
-treated seedlings, GA (Gibberellin acid)-treated
seedlings, JA (Jasmonic acid)-treated seedlings, ds-cDNA
molecules were generated as follows. First-strand cDNA was
prepared from oligo-dT selected mRNA by priming with a
NotI oligo-dT primer (5',
AAGCTGAGAAATTCGCGCCGACGAGCAATTTTTTTTTTTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA Pol- catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pTV3PAC vector. The library
then went through one round of normalization to Cop value
of 5 based on the methods of Marcello Bento Soares (Genome
Research 6: 791-806, 1996).
153 c 145 g 166 t

```

51.28;	Score 120.4;	DB 10;	Length 645;
ty 76.18;	Pred. No. 4.3e-24;		
ervative 0;	Mismatches 38;	Indels 0;	Gaps 0;

aagcctcggtgacagatcgcagcgtgcccatgctgataatgtgacggtcc 600
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
AGCATCGGTGACAGATCGACGCTGCCCATGCTGATAATGGACGGTCC 15

tcgctgtgtatctaattgttataattgagcagacacaacacgtacgt 12
|||||
|||
TCGTTGTGTTAATGTGTATAATTGAGCAGACACACACAGTACGT 95

[illegible]

11.univ ISUM5-RN Zea mays CNA clone MEST400-E11 3' mRNA
745 bp linear EST 18-DEC-2001

Phyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
nicoidae; Andropogoneae; Zea.
1 to 745)

sequence Tags from B73 Maize: various stages and tissue seedlings treated with a variety of hormones (2001)

nommy, Iowa State University, Ames, IA 50011-1010, USA

ORIGIN

Query Match 45.7%; Score 107.4; DB 9; Length 492;
Best Local Similarity 98.3%; Pred. No. 2e-20;

Matches 119; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 gtttcgcgtacgctcgtgagacagatcagcgtccatctgtatgaatgagcgttc 60
|||||
Db 141 GTTTCGCTACGCTCGGTGAGACAGATCAGCCTCCCTGATTAATGACGCTCC 82
|||||
QY 61 tgaatcattgctcgtgtgtatgaatgattgataatgagcagacacacgttact 120
|||||
Db 81 TGATTCATTGCTGCTGTGTATTATTAATGATGCA-CAGGACACACACGATACGT 23
|||||
QY 121 t 121
|
Db 22 T 22

RESULT 23

BM079887/c

LOCUS BM079887 530 bp mRNA linear EST 14-NOV-2001
DEFINITION MEST101-A03.T3 ISUM4-TN Zea mays cDNA clone MEST101-A03 3', mRNA
Sequence.

ACCESSION

BM079887

VERSION BM079887.1 GI:16926819

KEYWORDS

EST.

SOURCE

Zea mays.

ORGANISM

Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 530)

Qiu,F., Cui,F., Guo,L., Ashlock,D.A., Wen,T.J. and Schnable,P.S.
Expressed Sequence Tags from B73 Maize Seedlings and Silks

Unpublished (2001)

Contact: Patrick S. Schnable

JOURNAL

Unpublished (2001)

COMMENT

Unpublished (2001)

Schnable Laboratory
Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299

Email: schnable@iastate.edu

Individual basecall and confidence value were assigned using the
phred software,

(<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#
rt). Overall sequence quality assessment and vector trimming were

conducted using the Lucy software (<http://www.tigr.org/softlab/>).

Lucy parameters were set to ensure an overall trimmed quality of

97.5% or better without any vector fragments in the chosen

high-quality region of each sequence. Low-quality bases between the

poly-T and the high-quality region were replaced with N's to serve

as spacers.

PCR Primers

FORWARD: Forward PCR primer sequence, primer T7-1 (AA TAC GAC TCA

CTA TAG)

BACKWARD: Backward PCR primer sequence, primer T3 (ATT AAC CCT CAC

TAA AG)

Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

Location/Qualifiers

1..530

/organism="Zea mays"

/cultivar="B73"

/db_xref="taxon:4577"

/clone="MEST101-A03"

/clone_id="ISUM4-TN"

/tissue_type="Seedling and silk"

/lab_host="DH10B"

/note="Vector: pT73PAC; Site_1: EcoRI; Site_2: NotI;

ds-cDNA molecules were generated as follows. First-strand

cDNA was prepared from oligo-dT selected mRNA by priming

with a NotI oligo-dT primer (5',

AACTGACAGATTCCGGCCGACGAGATTTTTTTTTTTTTT). The
resulting DNA:RNA hybrid was treated with RNase H and used
as a template for DNA PolI-catalyzed second strand
synthesis. After the addition of EcoRI adaptors, the
ds-cDNAs were digested with NotI and size-selected. The
resulting molecules were directionally cloned into the
EcoRI and NotI sites of the pT73PAC vector. The library
then went through one round of normalization to Cot value
of 5 based on the methods of Marcelo Bento Soares (Genome
Research 6: 791-806, 1996)."

BASE COUNT

144 a 124 c 121 g 141 t

ORIGIN

Query Match 44.2%; Score 103.8; DB 10; Length 530;
Best Local Similarity 96.7%; Pred. No. 2.2e-19;

Matches 117; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 1 gtttcgcgtacgctcgtgagacagatcagcgtccatctgtatgaatgagcgttc 60
|||||
Db 142 GTTTCGCTACGCTCGGTGAGACAGATCAGCCTCCCTGATTAATGACGCTCC 83
|||||
QY 61 tgaatcattgctcgtgtgtatgaatgattgataatgagcagacacacgttact 120
|||||
Db 82 TGATTCATTGCTGCTGTGTATTATTAATGATGCA-CAGGACACACACGATACGT 25
|||||
QY 121 t 121
|
Db 24 T 24

RESULT 24

BM336874/c

LOCUS BM336874 435 bp mRNA linear EST 16-JAN-2002
DEFINITION MEST200-A08.T3 ISUM5-RN Zea mays cDNA clone MEST200-A08 3', mRNA
Sequence.

ACCESSION

BM336874

VERSION BM336874.1 GI:18167035

KEYWORDS

EST.

SOURCE

Zea mays.

ORGANISM

Zea mays.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 435)

Wen,T.J., Qiu,F., Guo,L., Ashlock,D.A. and Schnable,P.S.
Expressed Sequence Tags from B73 Maize: various stages and tissues

including seedlings treated with a variety of hormones

Unpublished (2001)

Contact: Patrick S. Schnable

JOURNAL

Unpublished (2001)

COMMENT

Unpublished (2001)

Schnable Laboratory
Iowa State University
G405 Agronomy, Iowa State University, Ames, IA 50011-1010, USA
Tel: 515-294-0975
Fax: 515-294-2299

Email: schnable@iastate.edu

Individual basecall and confidence value were assigned using the
phred software,

(<http://depts.washington.edu/ventures/collabtr/direct/index.htm>#
rt). Overall sequence quality assessment and vector trimming were

conducted using the Lucy software (<http://www.tigr.org/softlab/>).

Lucy parameters were set to ensure an overall trimmed quality of

97.5% or better without any vector fragments in the chosen

high-quality region of each sequence. Low-quality bases between the

poly-T and the high-quality region were replaced with N's to serve

as spacers.

PCR Primers

FORWARD: primer T7-1 (AA TAC GAC TCA CTA TAG)

BACKWARD: primer T3 (ATT AAC CCT CAC TAA AG)

Seq primer: primer T3 (ATT AAC CCT CAC TAA AG).

Location/Qualifiers

1..435

/organism="Zea mays"

FEATURES

source

Qy 143 nnnnnnnnnnnnnnc 159
 Db 72 TTGCATGCATCTCTC 56

RESULT 28
 AI901593 409 bp mRNA linear EST 27-JUL-1999
 LOCUS AI901593/c
 DEFINITION 618007E09.x1 618 - Inbred Tassel cDNA Library Zea mays cDNA, mRNA
 sequence.
 ACCESSION AI901593
 VERSION AI901593
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays.

REFERENCE
 AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 618007 row: E column: 09.
 Location/Qualifiers
 1. 409
 /organism="Zea mays"
 /cultivar="Ohio43"
 /db_xref="taxon:4577"
 /clone_lib="618 - Inbred Tassel cDNA Library"
 /tissue_type="tassel"
 /dev_stage="tassel length from 0.1 to 2.5 cm"
 /lab_host="XOLR"
 /note="Organ: tassel; Vector: PAD-GAL4-2.1 (Hybridzap);
 Inbred tassel library from Schmidt lab"

BASE COUNT 120 a 97 c 93 g 99 t

ORIGIN

Query Match 41.7%; Score 98; DB 9; Length 409;
 Best Local Similarity 100.0%; Pred. No. 9.4e-18;
 Matches 98; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtctccgtctagcctcggtgacagatcgacgtctgccatcgatgaatggacggtcc 60
 |||||||
 Db 98 GTTTCCGCTAGCCTCGGTGACAGATCGACGCTGCCCATCGCTGATTAATGGACGGTCC 39
 |||||||

Qy 61 tgatccatgtctgtgtatataatgtgtataat 98
 |||||||
 Db 38 TGATCATTGTCTGCTGTATATATGCTATTAAT 1

RESULT 29
 AI714565 581 bp mRNA linear EST 02-FEB-2000
 LOCUS AI714565/c
 DEFINITION 605059E11.x1 605 - Endosperm cDNA library from Schmidt lab Zea mays
 cDNA, mRNA sequence.
 ACCESSION AI714565
 VERSION AI714565.1
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays.

REFERENCE
 AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 614042 row: B column: 09.
 Location/Qualifiers
 1. 411
 /organism="Zea mays"
 /cultivar="W23"
 /db_xref="taxon:4577"
 /clone_lib="614 - root cDNA library from Walbot lab"

AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 605059 row: E column: 11.
 Location/Qualifiers
 1. 581
 /organism="Zea mays"
 /cultivar="Ohio43"
 /db_xref="taxon:4577"
 /clone_lib="605 - Endosperm cDNA library from Schmidt lab"
 /tissue_type="nucellar, embryo, and endosperm"
 /dev_stage="10-14 days post-pollination"
 /lab_host="DH5(alpha)"
 /note="Organ: kernel; Vector: PAD-GAL4-2'; Site_1: EcORI;
 Site_2: XhoI; kernel endosperm cDNA library from Schmidt
 lab"

BASE COUNT 155 a 148 c 138 g 140 t

ORIGIN

Query Match 36.2%; Score 85; DB 9; Length 581;
 Best Local Similarity 100.0%; Pred. No. 5.4e-14;
 Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 gtctccgtctagcctcggtgacagatcgacgtctgccatcgatgaatggacggtcc 60
 |||||||
 Db 85 GTTTCCGCTAGCCTCGGTGACAGATCGACGCTGCCCATCGCTGATTAATGGACGGTCC 26
 |||||||

Qy 61 tgatccatgtctgtgtatataatgtgtataat 85
 |||||||
 Db 25 TGATCATTGTCTGCTGTATATGCTATTA 1

RESULT 30
 AI978238 411 bp mRNA linear EST 27-AUG-1999
 LOCUS AI978238/c
 DEFINITION 614042B09.x2 614 - root cDNA library from Walbot lab Zea mays cDNA,
 mRNA sequence.
 ACCESSION AI978238
 VERSION AI978238.1
 KEYWORDS EST.
 SOURCE Zea mays.
 ORGANISM Zea mays.

REFERENCE
 AUTHORS Walbot,V.
 TITLE Maize ESTs from various cDNA libraries sequenced at Stanford
 JOURNAL Unpublished (1999)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 614042 row: B column: 09.
 Location/Qualifiers
 1. 411
 /organism="Zea mays"
 /cultivar="W23"
 /db_xref="taxon:4577"
 /clone_lib="614 - root cDNA library from Walbot lab"

[illegible][illegible]

REFERENCE		Eukaryote:	Viridiplantae;	Streptophyta;	Embryophyta;	Tracheophyta
AUTHORS		Spermatophyta;	Magnoliophyta;	Liliopsida;	Poales;	Poaceae; PACC
TITLE		clade: Panicoideae; Andropogoneae; Zea.				
JOURNAL		Maize ESTs from various cDNA libraries sequenced at Stanford University				
COMMENT		Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 486093 row: H column: 12.				
FEATURES		location/Qualifiers				
source		. . 602 /organism="Zea mays" /cultivar="B73" /db_xref="taxon:4577" /clone_lib="486 - leaf primordia cDNA library from Hake lab" /tissue_type="leaf primordia" /dev_stage="P7-P11 leaf" /lab_host="E.coli XL1-Blue MFR" note="Organ: shoot; Vector: Lambda zap; Hake lab CDNA library."				
BASE COUNT		121 a	201 c	179 g	99 t	2 others
ORIGIN						
Query Match		32.4%;	Score 76.2;	DB 9;	Length 602;	
Best Local Similarity		65.5%;	Pred. No. 1.8e-11;			
Matches		78;	Conservative 0;	Mismatches 41;	Indels 0;	Gaps 0;
Dy	117	acgtttnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncaggttcatacgaaccgc	176			
Db	384	AGGATGTACATCACTCAACTCGACCCTGACAAGGGCGGCACACAGTTTCATCAACACGCCG	443			
Qy	177	cgcatacgccaccttgycgctgacgacgcgcgaacttcacctgcggagggtcatcaagcccc	235			
Dy	444	CGCATTACGGCCCATCTTGCGCGTGAAGACGCGCACCTTCACCTGNAGAGGGTGTCACACCCC	502			
RESULT	35					
B1388940/c						
LOCUS		949047F08.xl 949 - Juvenile leaf and shoot cDNA from Steve Moose				
DEFINITION		Zea mays cDNA, mRNA sequence.				
ACCESSION		B1388940				
VERSION		B1388940.1 GI:15080094				
KEYWORDS		EST.				
SOURCE		Zea mays.				
ORGANISM		Zea mays. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade: Panicoideae; Andropogoneae; Zea.				
REFERENCE		Maize ESTs from various cDNA libraries sequenced at Stanford				
AUTHORS		University				
TITLE		Unpublished (1999)				
JOURNAL		Contact: Walbot V				
COMMENT		Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 949047 row: F column: 08.				
FEATURES		location/Qualifiers				
source		. . 413				

	/organism="Zea mays" /cultivar="W64A" /db_xref="taxon:4577" /clone_lib="949 - Juvenile leaf and shoot cDNA from Steve Moose" /tissue_type="Immature leaf primordium and vegetative meristem" /dev_stage="4 stages from 3-13 days after imbibing" /lab_host="E. coli XL0LR" /note="Organ: Juvenile vegetative shoots; Vector: PAD-GAL4-2.1; Site.1: EcORI; Site.2: XhoI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcORI (5') and XhoI (3'), directional cloning into lambda Hybridzap vector from Stratagene. Tissue Sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil. 2. Basal 1.5 cm shoots 6 days after sowing - includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing."
BASE COUNT	86 a 119 c 109 g 99 t
ORIGIN	
Query Match	32.2%; Score 75.6; DB 10; Length 413; Best Local Similarity 65.5%; Pred. No. 2.4e-11; Matches 78; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
Oy	117 acgttnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncaaggltcatcaagccgc 176 Db
Db	348 AGGATGTGCACCACTCCAGCCTCGACAGAGGGCGGCAACAGGTTTCATCAAGGCCG 289
Oy	177 cgatacggcgacattgcccgtgaagaagcgacttcacctgcagagtgtcaagcccc 235
Db	288 CGCATACGCGCACATTGGCCGTGACGACGCCGACTTACCCTGGAGAGTGTCGAAGCCCC 230
RESULT 36	
LOCUS	A1738382 463 bp mRNA linear EST 02-FEB-2000
DEFINITION	606049CD6.x1 606 - Ear tissue cDNA library from Schmidt lab Zea
ACCESSION	mays CDNA, mRNA sequence.
VERSION	A1738382
KEYWORDS	A1738382.1 GI:5081225
SOURCE	EST.
ORGANISM	Zea mays. Zea mays. Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 463)
REFERENCE	Maize ESTs from various cDNA libraries sequenced at Stanford
AUTHORS	Walbot,V.
TITLE	Unpublished (1999)
JOURNAL	Contact: Walbot V
COMMENT	Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 606049 row: C column: 06. Location/Qualifiers 1..463
FEATURES	
source	/organism="Zea mays" /cultivar="B73" /db_xref="taxon:4577" /clone_lib="947 - 2 week shoot from Barkan lab" /tissue_type="leaf and stem, including leaf base" /dev_stage="2 week old seedling (3 leaves)" /lab_host="XL1-Blue" /note="Organ: shoot; Vector: Lambda ZAP (phagescript SK-); Site.1: EcORI; Site.2: XhoI; directionally cloned using Stratagene's Unizap XR cDNA cloning kit with the 5' end at the EcoRI site. The library represents 8 x 10e5 independent recombinant phage. The plants were greenhouse grown."
BASE COUNT	109 a 116 c 134 g 131 t
ORIGIN	
Query Match	32.2%; Score 75.6; DB 10; Length 490; Best Local Similarity 65.5%; Pred. No. 2.5e-11; Matches 78; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
Oy	117 acgttnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncaggttcacaagccgc 176 Db
Db	391 AGGATGTGCACCACTCAACCTCGACCTCGAAGAAGGGCGGCAACAGGTTATCAAGGCCG 332
Oy	177 cgatacggcgacattgcccgtgaagaagcgacttcacctgcagagtgtcaagcccc 235
Db	331 CGCATACGCGCACATTGGCCGTGACGACGCCGACTTACCCTGGAGAGTGTCGAAGCCCC 273
RESULT 37	
LOCUS	BG550028 490 bp mRNA linear EST 05-APR-2001
DEFINITION	947080E01.y2 947 - 2 week shoot from Barkan lab Zea mays cDNA, mRNA
ACCESSION	sequence.
VERSION	BG550028
KEYWORDS	BG550028.1 GI:13558672
SOURCE	EST.
ORGANISM	Zea mays. Zea mays. Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 490)
REFERENCE	Maize ESTs from various cDNA libraries sequenced at Stanford
AUTHORS	Walbot,V.
TITLE	Unpublished (1999)
JOURNAL	Contact: Walbot V
COMMENT	Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 947080 row: E column: 01. Location/Qualifiers 1..490
FEATURES	
source	/organism="Zea mays" /cultivar="B73" /db_xref="taxon:4577" /clone_lib="947 - 2 week shoot from Barkan lab" /tissue_type="leaf and stem, including leaf base" /dev_stage="2 week old seedling (3 leaves)" /lab_host="XL1-Blue" /note="Organ: shoot; Vector: Lambda ZAP (phagescript SK-); Site.1: EcORI; Site.2: XhoI; directionally cloned using Stratagene's Unizap XR cDNA cloning kit with the 5' end at the EcoRI site. The library represents 8 x 10e5 independent recombinant phage. The plants were greenhouse grown."
BASE COUNT	109 a 116 c 134 g 131 t
ORIGIN	
Query Match	32.2%; Score 75.6; DB 10; Length 490; Best Local Similarity 65.5%; Pred. No. 2.5e-11; Matches 78; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
Oy	117 acgttnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncaggttcacaagccgc 176 Db
Db	391 AGGATGTGCACCACTCAACCTCGACCTCGAAGAAGGGCGGCAACAGGTTATCAAGGCCG 332
Oy	177 cgatacggcgacattgcccgtgaagaagcgacttcacctgcagagtgtcaagcccc 235
Db	331 CGCATACGCGCACATTGGCCGTGACGACGCCGACTTACCCTGGAGAGTGTCGAAGCCCC 273

BASE COUNT	155 a	152 c	133 g	148 t
ORIGIN				

RESULT 43
BES11079/C

155 a 152 c 133 g 148 t

LOCUS	BES11079	591 bp	mRNA	linear	EST 07-AUG-2000	
DEFINITION	946057F06.x1.946 - tassels primordium prepared by Schmidt lab Zea mays CDNA, mRNA sequence.					
ACCESSION	BES11079					
VERSION	BES11079.1	GI:9732327				
KEYWORDS	EST.					
SOURCE	Zea mays.					
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.					
REFERENCE	1 (bases 1 to 591)					
AUTHORS	Walbot,V.					
TITLE	Maze ESTs from various cDNA libraries sequenced at Stanford University					
JOURNAL	Unpublished (1999)					
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 946057 row: F column: 06. Location/Qualifiers 1..591 /organism="Zea mays" /cultivar="OH43" /db_xref="taxon:4577" /clone_lib="946 - tassels primordium prepared by Schmidt lab" /tissue_type="tassels" /dev_stage="just after the transition from vegetative to inflorescence development" /lab_host="XLDLR" /note="Organ: tassels; Vector: HybriZAP. Site_1: EcorI; Site_2: XhoI; George Chuck dissected immature tassels between 1mm and 3mm. Sharon Stanfield prepared the cDNA library in HybriZAP. Sample insert size range was 350 bp to 3 kb with a 1 Kb average." BASE COUNT 150 a 163 c 150 g 128 t ORIGIN					
Query Match	32.2%;	Score 75.6;	DB 10;	Length 591;		
Best Local Similarity	65.5%;	Pred. No. 2.6e-11;				
Matches	78;	Conservative	0;	Mismatches 41;	Indels 0;	
Gaps	0;					
Db	487 AGGGATGCTGCACCATCACTCGACCTTCAGAGAAGCGCGCACAGGTTCATCAAGACCGC	428				
OY	177 cgcatagcgacacttgccgtgacgacgcgacctcacctcgaagtggccaagcccc	235				
Db	427 CGCATAGCGGCCACTTTTGGCCGTGACGACGCCCGACTTCACTGGAGGGTGTCAGACCCC	369				
RESULT	44					
LOCUS	AM062087	632 bp	mRNA	linear	EST 05-OCT-1999	
DEFINITION	660009F01.y1.660 - Mixed stages of anther and pollen Zea mays CDNA, mRNA sequence.					
ACCESSION	AM062087					
VERSION	AM062087.1	GI:6012650				
KEYWORDS	EST.					
SOURCE	Zea mays.					
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.					
REFERENCE	1 (bases 1 to 632)					
AUTHORS	Walbot,V.					
TITLE	Maize ESTs from various cDNA libraries sequenced at Stanford					

JOURNAL	University Unpublished (1999)
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 660009 row: F column: 01. Location/Qualifiers 1..632 /organism="Zea mays" /cultivar="Ohio43" /db.xref="taxon:4577" /clone_id="660 - Mixed stages of anther and pollen" /tissue_type="whole premeiotic anthers to pollen shed" /dev_stage="premeiotic anthers to pollen shed" /lab_host="XJOLR" /note="Organ: anthers; Vector: Lambda Zap; Site_1: EcoRI; Site_2: XhoI; Ancher and pollen cDNA library. directionally sequenced with 5' end at the EcoRI site. Created by Ame Franklin."
FEATURES	
source	
BASE COUNT	155 a 149 c 163 g 164 t 1 others
ORIGIN	
Query Match	32.2%; Score 75.6; DB 9; Length 632;
Best Local Similarity	65.5%; Pred. No. 2,7e-11;
Matches	78; Conservative 0; Mismatches 41; Indels 0; Gaps 0;
Oy	117 acgtttnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnccaggttcacgaaccgc 176 Db 90 AGGATGTGCACCATCACTCGACTCAGAGGGCCGCAAGGTTTCATCACAGACC GC 149
Oy	177 cgcataggcgaacttgccgctgtagcgacggcacttcacctgcgagagtgcacaagcccc 235
Dd	150 CGCATACGCCACATTGGCCGCGTAGACGACCGCACTTCACTGGGAGGTGTCAAGCCCC 208
RESULT 45	A1920328 414 bp mRNA linear EST 29-JUL-1999
LOCUS	603019C04.xl 603 - stressed root cDNA library from Wang/Bohnert lab
DEFINITION	Zea mays CDNA, mRNA sequence.
ACCESSION	A1920328
VERSION	A1920328.1 GI:5649968
KEYWORDS	EST.
SOURCE	Zea mays.
ORGANISM	Eukaryotes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytas; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea. 1 (bases 1 to 414) Walbot, V Maize ESTs from various cDNA libraries sequenced at Stanford University Unpublished (1999) Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 603019 row: C column: 04. Location/Qualifiers 1..414 /organism="Zea mays" /cultivar="B73" /db.xref="taxon:4577" /clone_lib="603 - stressed root cDNA library from Wang/Bohnert lab"
JOURNAL	
COMMENT	
REFERENCE	
AUTHORS	
TITLE	
FEATURES	
source	

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/tissue_type="seedling"  
/dev_stage="salt stress"  
/lab_host="E. coli XL Gold"  
/note="Organ: root; Vector: pBluescriptII SK(+) XR;  
Seedling stressed root cDNA library from Wang/Bohnert lab"  
BASE COUNT      116 a      115 c      95 g      88 t  
ORIGIN
```

```
Query Match      32.1%; Score 75.4; DB 9; Length 414;  
Best Local Similarity 98.7%; Pred. No. 2.7e-11;  
Matches 76; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 159 caggttcacaaagaccgcccatacagccacitggccgtgacgagccgacttcacctg 218  
      |||  
Db 413 CAGGTCATCAAGACCGCCGCAATACGGCCACTTGGCCGTGACGACGCCGCACTTCACTG 354  
  
Qy 219 cgaagtggtcaagcccc 235  
      |||  
Db 353 GGAGGTGTCTCAAGCCCC 337
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Search completed: August 20, 2002, 00:55:59
Job time: 5984 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2002, 00:21:31 ; Search time 275.56 Seconds

(Without alignments)
1464.200 Million cell updates/sec

Title: US-09-198-779b-1

Perfect score: 235

Sequence: 1 gtttcgcgtacgtcgcgt.....ctgcgaggtgtgcaagcccc 235

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N.GeneSeq_032802.*

1: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT.*

2: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*

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11: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT.*

12: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT.*

13: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT.*

14: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT.*

15: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT.*

16: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT.*

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18: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT.*

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20: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT.*

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22: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT.*

23: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT.*

24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	121	51.5	2061	21	AAA48574	CDNA encoding corn
2	75.6	32.2	1674	21	AAc47744	Zea mays DNA fragment
3	65.8	28.0	1380	20	AAx07185	Wheat S-adenosylmethionine
4	61.6	26.2	1182	19	AAr99143	S-adenosylmethionine
5	61	26.0	1182	19	AAr99141	S-adenosylmethionine
6	59.4	25.3	1182	19	AAr99142	S-adenosylmethionine
7	54.6	23.2	399	20	AAx81128	S-adenosyl methionine
8	53	22.6	1485	20	AAx07184	Soybean S-adenosyl
9	53	22.6	1518	21	AAx51037	Soybean S-adenosyl

10	51	21.7	1582	20	AAx07183	Corn S-adenosylmet
11	50.4	21.4	635	21	AAc44219	Arabidopsis thalia
12	50.4	21.4	1508	21	AAc33986	Arabidopsis thalia
13	50.4	21.4	1521	21	AAc45478	Arabidopsis thalia
14	50.4	21.4	1529	21	AAc33535	Arabidopsis thalia
15	49.8	21.2	1653	21	AAc45944	Arabidopsis thalia
16	49.8	21.2	1654	21	AAc35348	Arabidopsis thalia
17	46.6	19.8	1636	22	AAc02226	Nicotiana tabacum
18	42.4	18.0	1393	21	AAc46421	Arabidopsis thalia
19	42.4	18.0	1395	21	AAc33674	Arabidopsis thalia
20	40.2	17.1	1208	15	AAc64204	snac gene encoding
21	40.2	17.1	5392	15	AAc64201	Sequence compislin
22	40	17.0	4848	24	AAc22684	Streptomyces fradi
23	39.4	16.8	1693	21	AAc75637	Streptomyces fradi
24	39.4	16.8	1693	21	AAc75637	Nucleotide sequenc
25	34.6	14.7	56485	21	AAx81476	Contig 004 from co
26	34.6	14.7	349980	21	AAc21612	N. meningitidis pa
27	34.6	14.7	837096	21	AAx81489	N. meningitidis pa
28	34.6	14.6	4403765	22	AAc199683	Mycobacterium tube
29	34.4	14.6	441529	22	AAc199682	Mycobacterium tube
30	34.4	14.0	17512	23	ABc09034	Drosophila melanog
31	31.2	13.3	1844	22	AAc99804	Human protein enco
32	30.8	13.1	66788	23	AAc59515	Pseudomonas aerugi
33	30.6	13.0	606	23	AAc51580	Aspergillus oryzae
34	30.6	13.0	657	21	AAc08427	Fusarium venenatum
35	30.6	12.9	566	21	AAc08427	GABA-gated chlorid
36	30.2	12.7	1519	20	AAc64373	Drosophila melanog
37	29.8	12.6	3550	23	ABc09035	CDNA encoding mugw
38	29.6	12.5	1683	18	AAc86246	Maize M109 protein
39	29.4	12.4	1557	21	AAc49567	CDNA encoding whea
40	29.2	12.4	2604	21	AAc48576	Corn encoding melano
41	29.2	12.4	1086	23	ABc04431	C glutaminc codin
42	29	12.3	1221	22	AAc66738	S-adenosylmethion
43	29	12.3	1221	22	AAc66738	Corynebacterium g1
44	29	12.3	1239	16	AAc04566	
45	29	12.3	1344	22	AAc71873	

ALIGNMENTS

RESULT 1	
AAA48574	AAA48574 standard; cDNA; 2061 BP.
ID	AAA48574
XX	XX
AC	AAA48574;
XX	XX
DT	19-SEP-2000 (first entry)
XX	XX
DE	CDNA encoding corn protein phosphatase 2A regulatory subunit A.
XX	XX
KW	Corn: protein phosphatase 2A; protein phosphorylation modulation;
KW	transgenic plant; gene therapy; ss.
XX	XX
OS	Zea mays.
XX	XX
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	56..1820
FT	/*tag- a
FT	/product= "protein phosphatase 2A regulatory
FT	subunit A"
XX	XX
PN	W0200036121-A2.
XX	XX
PD	22-JUN-2000.
XX	XX
PF	15-DEC-1999; 99WO-US29823.
XX	XX
PR	16-DEC-1998; 98US-0112541.
XX	XX
PA	(DUPC) DU PONT DE NEMOURS & CO E. I.
XX	XX
PI	Famodu OO, Miao G, Sakai H, Lee J, Rafalski JA, Klein TM;

XX MPI: 2000-431599/37.
DR P-PSDB: AAY9819.
XX
PT Polynucleotides encoding plant protein phosphatase useful for
PT modulating reversible protein phosphorylation in plants -
XX
PS Claim 4; Page 53-54; 73pp; English.
XX
CC The present sequence encodes corn protein phosphatase 2A regulatory
CC subunit A. The sequence was identified in clone p0018.chsuglor.fis of a
CC cDNA library made from corn ear shoot. BLAST analysis showed that the
CC present sequence encodes protein phosphatase 2A regulatory subunit A.
CC The sequence may be used for the recombinant production of the protein
CC in vivo, e.g. via a gene therapy protocol, or in vitro, e.g. in
CC fermentation culture. The protein may then be used to modulate the
CC process of reversible protein phosphorylation in plants. It may be used
CC directly to supplement a plant's own production of the enzyme or to
CC rectify mutations that result in the expression of inactive protein.
CC The protein may also be used to test for modulators of protein
CC phosphorylation which may be used to alter the activity of the enzyme.
XX
SQ Sequence 2061 BP; 549 A; 432 C; 498 G; 582 T; 0 other;

Query Match 51.5%; Score 121; DB 21; Length 2061;
Best Local Similarity 100.0%; Pred.No. 2.2e-31;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 gtttcgctctagctcgtgagacagatcagcgtccatgcatgataatgagcgtcc 60
Db 1908 gtttcgctctagctcgtgagacagatcagcgtccatgcatgataatgagcgtcc 1967
Oy 61 tgatccatgttcgctggtgtatataatgttataatgagcagacacacagctacgt 120
Db 1968 tgatccatgttcgctggtgtatataatgttataatgagcagacacacagctacgt 2027
Oy 121 t 121
Db 2028 t 2028

RESULT 2
AAC47744
ID AAC47744 standard; DNA; 1674 BP.
XX
AC AAC47744;
XX
DT 18-OCT-2000 (first entry)
XX
DE Zea mays DNA fragment SEQ ID NO: 54954.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic;
KW pathway; promoter; termination sequence; corn; ss.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 18-MAY-1999; 99US-0134370.
PR 19-MAY-1999; 99US-0134768.
PR 20-MAY-1999; 99US-0134941.
PR 21-MAY-1999; 99US-0135124.
PR 25-MAY-1999; 99US-0135353.
PR 25-MAY-1999; 99US-0135629.
PR 27-MAY-1999; 99US-0136021.
PR 28-MAY-1999; 99US-0136392.
PR 01-JUN-1999; 99US-0136782.
PR 03-JUN-1999; 99US-0137222.
PR 04-JUN-1999; 99US-0137528.
PR 07-JUN-1999; 99US-0137502.
PR 08-JUN-1999; 99US-0137724.
PR 10-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 16-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 17-JUN-1999; 99US-0139453.
PR 18-JUN-1999; 99US-0139482.
PR 18-JUN-1999; 99US-0139484.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139819.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140605.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142380.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.

PR	14-OCT-1999;	990S-0159320.
PR	14-OCT-1999;	990S-0159330.
PR	14-OCT-1999;	990S-0159331.
PR	14-OCT-1999;	990S-0159637.
PR	14-OCT-1999;	990S-0159638.
PR	18-OCT-1999;	990S-0159584.
PR	21-OCT-1999;	990S-0160741.
PR	21-OCT-1999;	990S-0160767.
PR	21-OCT-1999;	990S-0160768.
PR	21-OCT-1999;	990S-0160770.
PR	21-OCT-1999;	990S-0160814.
PR	21-OCT-1999;	990S-0160815.
PR	22-OCT-1999;	990S-0160980.
PR	22-OCT-1999;	990S-0160981.
PR	22-OCT-1999;	990S-0160989.
PR	25-OCT-1999;	990S-0161404.
PR	25-OCT-1999;	990S-0161405.
PR	25-OCT-1999;	990S-0161406.
PR	26-OCT-1999;	990S-0161359.
PR	26-OCT-1999;	990S-0161360.
PR	26-OCT-1999;	990S-0161361.
PR	28-OCT-1999;	990S-0161920.
PR	28-OCT-1999;	990S-0161992.
PR	28-OCT-1999;	990S-0161993.
PR	29-OCT-1999;	990S-0162142.

[illegible]

DR WPI: 1999-070263/06.
 DR P-PSDB: AAM97744.
 XX
 XX
 PT New plant amino acid biosynthetic enzymes, DNA and chimeric genes -
 PT encode: dihydropicolinate reductase; diaminopimelate epimerase;
 PT threonine synthase; threonine deaminase; S-adenosylmethionine
 synthetase
 XX

PS Claim 47; Page 69-70; 98pp; English.

CC This is the nucleotide sequence of a cDNA contig that codes for
 CC a full-length wheat S-adenosylmethionine synthetase (see AAM97744).
 CC The contig was assembled from clones isolated from wheat kernel,
 CC leaf, seedling and root cDNA libraries and identified by comparison
 CC to public sequence databases using BLAST algorithms. It shows
 CC sequence similarity to the barley enzyme. The invention relates to
 CC new isolated nucleic acid fragments (see AAM97168-85) encoding plant
 CC enzymes (see AAM97727-44) that catalyze steps in the biosynthesis of
 CC lysine, threonine, methionine, cysteine and isoleucine from
 CC aspartate, the enzyme being selected from dihydropicolinate reductase,
 CC diaminopimelate epimerase, threonine synthase, threonine deaminase
 CC or S-adenosylmethionine synthetase. The invention also relates to
 CC the construction of a chimeric gene encoding all or a portion of
 CC the biosynthetic pathway enzyme, in sense or antisense orientation,
 CC where expression of the chimeric gene results in production of
 CC altered levels of the enzyme in a transformed host cell.
 CC Overexpression or reduction of expression of genes encoding the
 CC amino acid biosynthetic pathway enzymes in crop plants such as
 CC corn, soybean and wheat can be used to alter levels of the amino
 CC acids in human food and animal feed. Transformed host cells can
 CC also be used to identify compounds that inhibit one of the enzymes.
 XX
 XX Sequence 1380 BP; 299 A; 430 C; 379 G; 267 T; 5 other;

Query Match 28.0%; Score 65.8; DB 20; Length 1380;
 Best Local Similarity 90.9%; Pred. No. 1.9e-12;
 Matches 70; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

OY 159 caggttcataagaccgcgcatacgcacattgcccgtgacgcgcgaacttaccctg 218
 ||||||||||||||||
 DB 1155 caggttcataagaccgcgcatacgcacattgcccgtgacgcgcgaacttaccctg 218
 ||||||||||||||||
 OY 219 cgagggtggtcaagccccc 235
 ||||||||
 DB 1215 ggaagggtggtgaagccccc 1231

RESULT 4

AAT99143
 ID AAT99143 standard; cDNA to mRNA; 1182 BP.

AC AAT99143;

DT 26-MAR-1998 (first entry)

DE S-adenosylmethionine synthase 3 gene.

XX S-adenosylmethionine synthase 3 gene; barley; alkali resistant plant;
 KW sam3; ss.

OS Hordeum vulgare.

PN JP09313186-A.

PD 09-DEC-1997.

PF 28-MAY-1996; 96JP-0133406.

PR 28-MAY-1996; 96JP-0133406.

PA (NIOC) NIPPON OIL CO LTD.

DR WPI: 1998-080077/08.
 DR P-PSDB: AAM34542.

XX S-adenosyl-methionine synthase gene - useful in producing plants
 PT resistant to alkaline soil
 XX

PS Claim 6; Page 10-11; 13pp; Japanese.

CC This sequence represents the S-adenosylmethionine synthase 3 (sam3)
 CC gene. This DNA sequence may be used in a vector to produce plants which
 CC are resistant to alkaline soil.
 XX

SO Sequence 1182 BP; 253 A; 368 C; 331 G; 230 T; 0 other;

Query Match 26.2%; Score 61.6; DB 19; Length 1182;
 Best Local Similarity 88.2%; Pred. No. 4.9e-11;
 Matches 67; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

OY 160 aggttcataagaccgcgcatacgcacattgcccgtgacgcgcgaacttaccctg 219
 ||||||||||||||||
 DB 1084 aggttcataagaccgcgcatacgcacattgcccgtgacgcgcgaacttaccctg 1143
 ||||||||||||||||
 OY 220 gaggtggtcaagccccc 235
 ||||||||
 DB 1144 gaggtggtgaagccccc 1159

RESULT 5

AAT99141
 ID AAT99141 standard; cDNA to mRNA; 1182 BP.

AC AAT99141;

DT 26-MAR-1998 (first entry)

DE S-adenosylmethionine synthase 1 gene.

KW S-adenosylmethionine synthase 1 gene; barley; alkali resistant plant;
 KW sam1; ss.

OS Hordeum vulgare.

PN JP09313186-A.

PD 09-DEC-1997.

PF 28-MAY-1996; 96JP-0133406.

PR 28-MAY-1996; 96JP-0133406.

PA (NIOC) NIPPON OIL CO LTD.

DR WPI: 1998-080077/08.

DR P-PSDB: AAM34540.

PT S-adenosyl-methionine synthase gene - useful in producing plants
 PT resistant to alkaline soil

PS Claim 4; Page 8-9; 13pp; Japanese.

CC This sequence represents the S-adenosylmethionine synthase 1 (sam1)
 CC gene. This DNA sequence may be used in a vector to produce plants which
 CC are resistant to alkaline soil.
 XX

SO Sequence 1182 BP; 253 A; 372 C; 324 G; 233 T; 0 other;

Query Match 26.0%; Score 61; DB 19; Length 1182;
 Best Local Similarity 87.0%; Pred. No. 7.8e-11;
 Matches 67; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 159 caggttcataagaccgcgcatacgcacattgcccgtgacgcgcgaacttaccctg 218

Db 1083 caggttcatacgaacagcgtctcactgctcacttggccgcgagatgctgacttaccctg 1142
 |||||||
 QY 219 cgaagtggtcaagccccc 235
 |||||||
 Db 1143 ggaagtggtgaagccccc 1159

RESULT 6

AAT99142
 ID AAT99142 standard; cDNA to mRNA; 1182 BP.

AC AAT99142;

DT 26-MAR-1998 (first entry)

DE S-adenosylmethionine synthase 2 gene.

KW S-adenosylmethionine synthase 2 gene; barley; alkali resistant plant;
 sam2; ss.

OS Hordeum vulgare.

PN JP09313186-A.

PD 09-DEC-1997.

PF 28-MAY-1996; 96JP-0133406.

PR 28-MAY-1996; 96JP-0133406.

PA (NIOC) NIPPON OIL CO LTD.

DR WPI: 1998-080077/08.

P-PSDB; AAM34541.

PT S-adenosyl-methionine synthase gene - useful in producing plants
 resistant to alkaline soil

PS Claim 5; Page 9-10; 13pp; Japanese.

CC This sequence represents the S-adenosylmethionine synthase 2 (sam2)
 CC gene. This DNA sequence may be used in a vector to produce plants which
 CC are resistant to alkaline soil.

SQ Sequence 1182 BP; 261 A; 368 C; 324 G; 229 T; 0 other;

Query Match 25.3%; Score 59.4; DB 19; Length 1182;
 Best Local Similarity 85.7%; Pred. No. 2.8e-10;
 Matches 66; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 159 caggttcatacgaacagcgtctcacttggccgcgagatgctgacttaccctg 218
 |||||||
 Db 1083 caggttcatacgaacagcgtctcacttggccgcgagatgctgacttaccctg 1142
 |||||||
 QY 219 cgaagtggtcaagccccc 235
 |||||||
 Db 1143 ggaagtggtgaagccccc 1159

RESULT 7

AAK81128
 ID AAK81128 standard; cDNA; 399 BP.

AC AAK81128;

DT 06-SEP-1999 (first entry)

DE S-adenosyl methionine (SAM) partial cDNA sequence.

KW Senescence-associated receptor-like protein kinase; sak; sam gene; sag;
 KM senescence-associated gene; plant senescence; promoter; pharmaceutical;

KW plant maturation; S-adenosyl methionine; flower; fruit development; ss.
 OS Phaseolus vulgaris.

PN WO929159-A1.

PD 17-JUN-1999.

PF 08-DEC-1998; 98MO-US25799.

PR 08-DEC-1997; 97US-0067898.

PA (VITA-) VITALITY BIOTECHNOLOGIES INC.

PI Gepstein S, Hajnóje T, Rosner A;

DR WPI: 1999-404873/34.

P-PSDB; AAY21978.

PT DNA encoding senescence-associated genes for a senescence
 PT receptor-like protein kinase

PS Claim 18; Fig 4; 70pp; English.

CC The invention relates to a senescence-associated receptor-like protein
 CC kinase (sak) gene. The sak gene is a senescence-associated gene (sag)
 CC and is expressed early in the plant senescence process. The sak gene
 CC promoter is useful for driving expression of foreign genes having a
 CC desired product, such as a pharmaceutical, during the process of plant
 CC maturation. The sak gene promoter can be used to drive expression of
 CC resistance genes against pathogens or pests during senescence when the
 CC plant is particularly susceptible to infection or infestation. The sak
 CC gene promoter may also be used to drive expression of a gene encoding an
 CC inhibitor of senescence. Plant senescence may be inhibited by use of
 CC antisense sak constructs. Over expression of the sag gene, using the
 CC sak or sam (S-adenosyl methionine) gene promoters is useful for
 CC induction of early senescence. This is useful to obtain flower or fruit
 CC development prior to specific pest onset, prior to undesirable cross-
 CC fertilization from related crops, at a specific time during storage or
 CC retail, or to avoid development of plant structures that are not of
 CC agronomic importance. The present sequence represents a partial cDNA
 CC clone of S-adenosyl methionine (SAM).

SQ Sequence 399 BP; 108 A; 80 C; 82 G; 129 T; 0 other;

Query Match 23.2%; Score 54.6; DB 20; Length 399;
 Best Local Similarity 81.8%; Pred. No. 7.8e-09;
 Matches 63; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 159 caggttcatacgaacagcgtctcacttggccgcgagatgctgacttaccctg 218
 |||||||
 Db 101 caggttcatacgaacagcgtctcacttggccgcgagatgctgacttaccctg 160
 |||||||
 QY 219 cgaagtggtcaagccccc 235
 |||||||
 Db 161 ggaagtggtgaagccccc 177

RESULT 8

AAK07184
 ID AAK07184 standard; cDNA; 1485 BP.

AC AAK07184;

DT 21-MAY-1999 (first entry)

DE soybean S-adenosylmethionine synthetase cDNA clone s2.12b06.

KW S-adenosylmethionine synthetase; soybean; amino acid; lysine;
 KM threonine; methionine; cysteine; isoleucine; transgenic plant;
 crop improvement; food; feedstuff; ss.

[illegible]

XX	09-OCt-2000	(first entry)
XX		
DE	Soybean S-adenosyl-L-methionine synthetase cDNA.	
XX		
KM	S-adenosyl-L-methionine synthetase; SAMS; probe; promoter; embryo;	
KW	constitutive; tissue-specific; development-specific;	
XX	herbicide resistance; pathogen resistance; ss.	
XX		
OS	Glycine max.	
XX		
FH	Key	Location/Qualifiers
FT	5'UTR	1..73
FT		/*tag= a
FT	CDS	74..1252
FT		/*tag= b
FT		/product= S-adenosyl-L-methionine_Synthetase
PN	W0200037662-A2.	
XX		
PD	29-JUN-2000.	
XX		
PF	17-DEC-1999;	99MO-US30180.
XX		
PR	21-DEC-1998;	98US-0113045.
XX		
PA	(DUPO) DU PONT DE NEMOURS & CO E. I.	
XX		
PI	Falco SC, Li Z;	
XX		
DR	WPI; 2000-442682/38.	
XX		
PT	S-adenosyl-L-methionine synthetase promoter for expressing target	
PT	heterologous herbicide-resistance or pathogen-resistance nucleic acid	
PS	fragments in plants, especially soybean	
XX		
PS	Example 2; Page 39; 50pp; English.	
XX		
CC	This is the soybean full-length S-adenosyl-L-methionine synthetase (SAMS)	
CC	cDNA, which was used to generate a probe to isolate a SAMS promoter. The	
CC	SAMS promoter is active in seedlings and callus and over-expression of a	
CC	gene in embryo stage can be achieved at an early developing stage using	
CC	the SAMS promoter. The SAMS promoter may be used as an alternative to	
CC	cauliflower mosaic virus 35S promoter to drive expression of selectable	
CC	marker genes. Plant cells transformed with the SAMS constitutive promoter	
CC	are useful for increasing or decreasing the expression of heterologous	
CC	nucleic acid fragments in a plant, preferably corn, rice, wheat, barley,	
CC	palm, Arabidopsis, soybean, oil seed Brassica, peanut, sunflower,	
CC	safflower, cotton, tobacco, tomato, potato or cocoa. Target heterologous	
CC	nucleic acid fragments include herbicide or pathogen resistance	
CC	nucleic acid fragments.	
XX		
XX		
SQ	Sequence 1518 BP; 399 A; 373 C; 357 G; 389 T; 0 other;	
	Query Match	22.6%; Score 53; DB 21; Length 1518;
	Best Local Similarity	80.5%; Pred. No. 5e-08;
	Matches	62; Conservative 0; Mismatches 15; Indels 0; Gaps 0.
QY	139 caggttcacaaagccgcatacgaacatttgccgtgacgaagccagcttcacatg	218
DB	1156 caggttcctgaagctgctcatagacactcgacagagagacccctgacttcacatg	1215
QY	219 cgagtggtcgaagcccc	235
DB	1216 ggaagtggtcgaagcccc	1232
RESULT	10	
ID	AAK07183	
XX	AAK07183 standard; cDNA; 1582 BP.	
XX		
CC	AAK07183;	

XX 21-MAY-1999 (first entry)
XX
DE Corn S-adenosylmethionine synthetase cDNA clone cc3.mn0002.d2.
XX
XX S-adenosylmethionine synthetase; corn; maize; amino acid; lysine;
KW threonine; methionine; cysteine; isoleucine; transgenic plant;
KW crop improvement; food; feedstuff; ss.
XX
OS Zea mays.
XX
FH Key Location/Qualifiers
FT CDS 140..1330
FT /*tag= a
XX
XX MO9855601.A2.
XX PD 10-DEC-1998.
XX
XX PF 05-JUN-1998; 98MO-US11692.
XX
XX PR 12-JUN-1997; 97US-0049443.
XX PR 06-JUN-1997; 97US-0048771.
XX
XX PA (DUP0) DU PONT DE NEMOURS & CO E. I.
XX
XX PI Abell LM, Allen SM, Falco SC, Hltz WD, Kinney AJ;
XX PI Rafalski JA, Thorpe CJ;
XX
XX WPI; 1999-070263/06.
XX P-PSDB; AAW97742.
XX
XX New plant amino acid biosynthetic enzymes, DNA and chimeric genes -
PT encode: dihydrotropicolinate reductase; diaminopimelate epimerase;
PT threonine synthase; threonine deaminase; S-adenosylmethionine
PT synthetase
XX
XX Claim 41; Page 62-63; 98pp; English.
XX
XX This is the nucleotide sequence of cDNA clone cc3.mn0002.d2, which
XX codes for a full-length corn S-adenosylmethionine synthetase
XX (see AAW97742). The clone was isolated from a corn callus cDNA
XX library and identified by comparison to public sequence databases
XX using BLAST algorithms. It shows sequence similarity to the
XX Oryza sativa enzyme. The invention relates to new isolated
XX nucleic acid fragments (see AAX07168-85) encoding plant enzymes (see
XX AAW97727-44) that catalyze steps in the biosynthesis of lysine, the
XX threonine, methionine, cysteine and isoleucine from aspartate, the
XX enzyme being selected for dihydrotropicolinate reductase,
XX diaminopimelate epimerase, threonine synthase, threonine deaminase
XX or S-adenosylmethionine synthetase. The invention also relates to
XX the construction of a chimeric gene encoding all or a portion of
XX the biosynthetic pathway enzyme. In sense or antisense orientation,
XX where expression of the chimeric gene results in production of
XX altered levels of the enzyme in a transformed host cell.
XX Overexpression or reduction of expression of genes encoding the
XX amino acid biosynthetic pathway enzymes in crop plants such as
XX corn, soybean and wheat can be used to alter levels of the amino
XX acids in human food and animal feed. Transformed host cells can
XX also be used to identify compounds that inhibit one of the enzymes.
XX
XX Sequence 1582 BP; 340 A; 474 C; 417 G; 351 T; 0 other;

Query Match 21.7%; Score 51; DB 20; Length 1582;
Best Local Similarity 80.0%; Pred. No. 2.5e-07;
Matches 60; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

OY 161 gttcatcaagacgcgcacttgccgtgacgacgcgacttaccctgcg 220
DB 1230 gctacccaagacgcgcacttgccgtgacgacgcgacttaccctgcg 1289
OY 221 agtgtgtcaagcccc 235

DB 1290 agtgtgtcaagcccc 1304
|||||
RESULT 11
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ID AAC44219 standard; DNA: 635 BP.
XX
XX AAC44219;
XX
XX 18-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 42062.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
XX
XX PN EP1033405-A2.
XX
XX PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX PF 25-FEB-1999; 99US-0121825.
XX PR 05-MAR-1999; 99US-0123180.
XX PR 09-MAR-1999; 99US-0123548.
XX PR 23-MAR-1999; 99US-0125788.
XX PR 29-MAR-1999; 99US-0126264.
XX PR 01-APR-1999; 99US-0126785.
XX PR 06-APR-1999; 99US-0127462.
XX PR 08-APR-1999; 99US-0128234.
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XX PR 21-APR-1999; 99US-0130077.
XX PR 23-APR-1999; 99US-0130510.
XX PR 28-APR-1999; 99US-0130891.
XX PR 30-APR-1999; 99US-0131449.
XX PR 04-MAY-1999; 99US-0132407.
XX PR 05-MAY-1999; 99US-0132484.
XX PR 06-MAY-1999; 99US-0132485.
XX PR 06-MAY-1999; 99US-0132486.
XX PR 06-MAY-1999; 99US-0132487.
XX PR 07-MAY-1999; 99US-0132863.
XX PR 11-MAY-1999; 99US-0134256.
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XX PR 20-MAY-1999; 99US-0135124.
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XX PR 24-MAY-1999; 99US-0135629.
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XX PR 01-JUN-1999; 99US-0137222.
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XX PR 08-JUN-1999; 99US-0138094.
XX PR 10-JUN-1999; 99US-0138540.
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PR	14-OCT-1999;	9905-0159295
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PR	29-OCT-1999;	9905-0162142

Query Match	21.4%;	Score 50.4;	DB 21;	length 635;
Best Local Similarity	78.9%;	Pred. No. 2.7e-07;		
Matches 60;	Conservative 0;	Mismatches 16;	Indels 0;	Gaps 0;

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QY	163		
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QY	171		
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QY	174		
QY	175		
QY	176		
QY	177		
QY	178		
QY	179		
QY	180		
QY	181		
QY	182	aggtctcttgaagacgcgcgcctatggttaactttgaaagggacgatgtctgatttcaactgc	341
QY	183		
QY	184		
QY	185		
QY	186		
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QY	200	gaggtgtgtcaagccccc	235
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QY			

RESULT 12
AAC33986
ID AAC33986 standard; DNA; 1508 BP.
XX
AC AAC33986;
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 5035.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
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PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
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PR 29-MAR-1999; 99US-0126785.
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PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
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PR 29-OCT-1999; 99US-0162142.

Query Match 21.4%; Score 50.4; DB 21; Length 1508;
Best Local Similarity 78.9%; Pred. No. 3.9e-07;
Matches 60; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
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Db 1170 aggttcttgaagactgctctatgctacattggaagagcagatgctgattcacctcg 1229
Qy 220 gagtggatcaagccgc 235
Db 1230 gagtgaatcaagccac 1245

RESULT 13
AAC45478

ID AAC45478 standard; DNA; 1521 BP.
XX
AC AAC45478;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 46638.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 16-APR-1999; 99US-0128714.
PR 19-APR-1999; 99US-0130077.
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PR 18-JUN-1999; 99US-0139460.


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XX 17-OCT-2000 (first entry)
DT
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 3408.
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XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
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XX EPI03405-A2.
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XX 06-SEP-2000.
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XX 25-FEB-2000; 2000EP-0301439.
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PR 29-OCT-1999; 99US-0162142.
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Query Match 21.4%; Score 50.4; DB 21; Length 1529;
Best Local Similarity 78.9%; Pred. No. 3.9e-07;
Matches 60; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
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OY 220 gaggtggtcaagccc 235
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Db 1270 gaagtcgtcaagccac 1285
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RESULT 15
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ID AAC45944 standard; DNA; 1653 BP.
XX
AC AAC45944;
XX
DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana DNA fragment SEQ ID NO: 48340.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
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OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 29-OCT-1999; 99US-0162142.

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RESULT 16
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DT 17-OCT-2000 (first entry)
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KW Hybridisation assay; genetic mapping; gene expression control;
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PR 29-OCT-1999; 99US-0162142.

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Query March 21.2%; Score 49.8; DB 21; Length 1654;
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Db 1288 ggaagtgttcaagccgc 1304

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RESULT 17
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ID AAD02296 standard; DNA; 1636 BP.
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AC AAD02296;
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DT 28-MAR-2001 (first entry)
XX
DE Nicotiana tabacum S-adenosylmethionine synthetase (SAMS) DNA.
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KW Tobacco; alkaloid; nicotine; transgenic plant; pharmaceutical protein;
herbicide resistance; S-adenosylmethionine synthetase; SAMS; ds.
XX
OS Nicotiana tabacum.

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XX Key Location/Qualifiers
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PN WO200067558-A1.
XX
PD 16-NOV-2000.
XX
PF 05-MAY-2000; 2000MO-US12450.
XX
PR 06-MAY-1999; 99US-0132919.
XX
PA (TIMK/) TIMKO M.
XX
PI Timko M;
XX
DR WPT, 2001-007279/01.
XX
DR P-PSDB; AAV72078.
XX
PT New nucleic acid encoding alkaloid-synthesis enzymes in tobacco, useful
PT e.g. for producing transgenic plants with altered nicotine content.
XX
PS Claim 1: Page 78-79; 103pp; English.
XX
CC The invention relates to enzymes involved in alkaloid, specifically
CC nicotine, synthesis in tobacco and nucleic acids encoding them. The
CC nucleic acid of the invention can be used, in sense or antisense
CC orientation, to produce transgenic tobacco plants with altered
CC alkaloid content, and also for expression of exogenous proteins,
CC e.g. pharmaceutical proteins or proteins implicated in resistance
CC to herbicides. The protein of the invention can be used to
CC identify modulators of enzymatic activity in plants.
CC The present sequence is Nicotiana tabacum S-adenosylmethionine
CC synthetase (SAMS) DNA. This enzyme is involved in the nicotine
CC biosynthetic pathway.
XX
SQ Sequence 1636 BP; 444 A; 365 C; 373 G; 454 T; 0 other;

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Query Match 19.8%; Score 46.6; DB 22; Length 1636;
Best Local Similarity 75.3%; Pred. No. 8.2e-06;
Matches 58; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Db 1175 cagttaccagaagactgagacttatgtcacttggccgtgatgaccccgacttctatg 1234
QY 219 cgaagtgtgtaagccccc 235
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Db 1235 ggaagtgttcaagttcc 1251

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RESULT 18
AAC46421
ID AAC46421 standard; DNA; 1393 BP.
XX
AC AAC46421;
XX

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DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 50076.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
protein identification; signal transduction pathway;
metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX

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PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 22-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.
PR 29-OCT-1999; 99US-0162143.
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Query Match 18.0%; Score 42.4; DB 21; Length 1393;
Best Local Similarity 72.4%; Pred. No. 0.00021;
Matches 55; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
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QY 160 aggttcataagacgcgcgaacattgcccgtgaagcgcgacttcacccg 219
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Db 1175 aggttcgaaacgcgcgcgtatcgacattcggaagagacgcgcgacttcacccg 1234
QY 220 gaggtggtcaagccccc 235
      |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1235 gaggtcgtgaagccac 1250
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RESULT 19
AAC33674
ID AAC33674 standard; DNA; 1395 BP.
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AAC33674:

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 3906.

XX Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

XX metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.

PN EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

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XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
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PR 06-MAY-1999; 99US-0132486.
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PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134376.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 21-MAY-1999; 99US-0135629.
PR 24-MAY-1999; 99US-0136021.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136782.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
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PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
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PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139889.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
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PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
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PR 15-JUL-1999; 99US-0144005.
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PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
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PR 17-AUG-1999; 99US-0149175.
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PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149722.
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PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 30-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.

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PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
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PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
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PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
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PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
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PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161993.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match      18.0%; Score 42.4; DB 21; Length 1395;
Best Local Similarity 72.4%; Pred. No. 0.00021;
Matches 55; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

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Oy 160 aggttcataaagacgcgcgcataagcgcatttgccgtgacgacgcgaacttcacccgc 219
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Db 1175 aggttcagaaacgcgcgcgtatgacatttcggaagacgacgccttaccctcg 1234
Oy 220 gaggtggtcaagccccc 235
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 1235 gaggtcgtcaagccac 1250

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RESULT 20
AA064204
ID AA064204 standard; cDNA: 1208 BP.
XX
XX AA064204;
AC
XX
XX 18-NOV-1994 (first entry)
DT
XX
XX snac gene encoding enzyme in streptogramin biosynthetic pathway.
DE
XX
XX Antibiotic: streptogramin; snac; snac; snac; biosynthesis: enzyme;
KW biosynthetic pathway; Streptomyces pristinaespiralis; ds.
XX
OS Streptomyces pristinaespiralis.
XX
XX Key Location/Qualifiers
FH CDS 1..1209
FT /*tag= a
XX
XX FR2696189-A.
XX 01-APR-1994.
PD
XX 25-SEP-1992; 92FR-0011441.
PF

```

```

PI Blanc V, Branche F, Crouzet J, Jacques N, Lacroix P;
PI Thibaut D, Zagorec M;
DR WPI: 1994-128286/16.
XX DNA involved in streptogramin antibiotic biosynthesis - for
PT prodn. or bio-conversion of streptogramin(s) or prodn. of
PT streptogramin intermediates, derivs. or hybrid antibiotics
PS Disclosure; Page 44-47; 83pp; French.
XX
CC This sequence comprises the snaA, snab and snac genes which are
CC involved in the biosynthesis of streptogramins, antibiotics active
CC against Gram-positive bacteria. The identification of the sequences
CC encoding the enzymes involved in the biosynthetic pathway means that
CC they can be isolated and manipulated. Mutant microorganisms in
CC which a step in the streptogramin biosynthetic pathway is blocked
CC can be cultured to produce streptogramin intermediates, which may
CC later be converted to streptogramin derivatives. Recombinant cells
CC may also be used for the bioconversion of streptogramins from one
CC form to another or for the production of hybrid antibiotics.
CX
SQ Sequence 5392 BP; 811 A; 2161 C; 1671 G; 749 T; 0 other;

Query Match      17 1%; Score 40.2; DB 15; Length 5392;
Best Local Similarity 46.7%; Pred. No. 0.0022;
Matches 57; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

QY 113 acgtacgttannnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncagttcataaga 172
   || | |
DB 4612 acctgcgccccggcgcatatccgacccttcgcactgcgtcggcccatctaagccgccca 4671
   ||||| |

QY 173 ccgcgcatacgaaggcaatttgccgtgtagcagccgcagcatcacctgcagagtgtccaagc 232
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DB 4672 ccgcgcatacgaaggcaatttcgcgcgagacctgcgcactcactcgtgagcagcagcagcc 4731
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QY 233 cc 234
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DB 4732 gc 4733

RESULT 22
AAD22684
ID AAD22684 standard; DNA; 4848 BP.
XX
AC AAD22684;
XX
DT 26-FEB-2002 (first entry)
XX
DE Streptomycetes fradiiae S-adenosylmethionine (SAM) operon DNA.
XX
KM S-adenosylmethionine; SAM operon; SAM synthetase; methyltransferase;
KW MT; methylene tetrahydrofolate reductase; MTHFR; activated methyl cycle;
  lysotin production; ds.
XX
OS Streptomycetes fradiiae.
XX
FH Key Location/Qualifiers
FT CDS 986..2209
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   /product= "SAM synthetase protein"
   2241..3341
   /*tag= b
   /product= "methyltransferase protein"
   /transl_except= (2241..2243, aa:Met)
   3358..4255
   /*tag= c
   /product= "methylene tetrahydrofolate reductase protein"
   /transl_except= (3358..3340, aa:Met)
FT
FT
XX US6312920-B1.
```

PI		Dehoff BS, Rosteck PR;
XX		
DR		WPI; 2002-024904/03.
XX		
PT		New S-adenosylmethionine (SAM) operon from Streptomyces fradiae which
PT		tetracycline SAM synthetase, methyltransferase and methylene
PT		tetrahydrofolate reductase, useful for producing SAM by recombinant
PT		techniques -
XX		
PS		Claim 19; Column 31-36; 22pp; English.
XX		
CC		The patent discloses Streptomyces fradiae S-adenosylmethionine (SAM)
CC		operon which comprises three genes encoding SAM synthetase, methyl-
CC		transferase (MT) and methylene tetrahydrofolate reductase (MTHFR).
CC		SAM synthetase, MT and MTHFR together comprise the activated methyl
CC		cycle which produces SAM and provides methyl groups required for
CC		the final steps in tylosin production. The invention also relates
CC		to vectors and transformed heterologous host cells for expressing
CC		SAM synthetase. It also relates to a method useful for producing
CC		SAM by recombinant techniques. The present mRNA sequence is SAM
CC		operon from Streptomyces fradiae.
XX		
SQ		Sequence 4848 BP; 648 A; 1869 C; 1696 G; 635 U; 0 other;
XX		
Query Match		17.0%; Score 40; DB 24; Length 4848;
Best Local Similarity		40.4%; Pred. No. 0.0025;
Matches	44;	Conservative 8; Mismatches 57; Indels 0; Gaps
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Db	2055	accucgcgccgcccgcgcgaucacggcgauucggacucgcgcgcgcgaucacgcaaa 211
OY	173	cgcgcgatcacgccacttcgcgcgttacaagcgcgcattcactcgcga 221
		: : : : :
Db	2115	cgcgcgcuaacgcgcacucugcgcgcgcgaacucgccgguuacucugga 2163
XX		
RESULT 24		
AAAT5637/c		
ID	AAA75637	standard; DNA; 1693 BP.
XX		
AC	AAA75637;	
XX		
DT	22-JAN-2001	(first entry)
DE		
Nucleotide sequence of ORF15 encoding S-adenosylmethionine synthetase		
KM	Narhopolide synthase; polyketide synthase gene; narhopolide polyketid	
KM	antibiotic; C12-hydroxylase; pik; desosamine biosynthesis;	
KM	desosaminyl transferase enzyme; ketolide; beta-glucosidase enzyme;	
KM	pictorycin biosynthesis; ss.	
XX		
OS	Streptomyces venezuelae.	
XX		
PN	US6117659-A.	
XX		
PD	12-SEP-2000.	
XX		
PF	27-MAY-1999;	9905-0320878.
XX		
PR	28-MAY-1998;	9805-0087080.
PR	22-SEP-1998;	9805-0100880.
PR	08-FEB-1999;	9905-0119139.
PR	20-MAY-1999;	9905-0134990.
PR	30-APR-1997;	9705-0846247.
PR	06-MAY-1998;	9805-0073538.
PR	28-AUG-1998;	9805-0141908.
XX		
PA	(KOSA-) KOSAN BIOSCIENCES INC.	
XX	Ashley G, Betlach MC, Betlach M, Tang L, McDaniel R;	
XX		


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Db 452410 ACCTGCGCCCAAAAGGCAATGCTCCAAATGCTGATCTCTTGCGCCGCAATTTACAGTAAT 452351
QY 173 ccgcgcgcatacgcgcacatttgccgtagcagacgcgcactcaactgcgaq 222
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Db 452350 CCGCGCGCTTAGGACATTTCGGCGCGGAGAACCTGATTCACTTGGGAG 452301

RESULT 29
AA199683
ID AA199683 standard; DNA: 4403765 BP.
XX
AC AA199683;
XX
DT 15-JUN-2002 (first entry)
XX
DE Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 2.
XX
KW Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome;
XX variation; epidemiology; patient treatment; epidemic monitoring; ds.
XX
OS Mycobacterium tuberculosis.
XX
PN US6294328-B1.
XX
PD 25-SEP-2001.
XX
PF 24-JUN-1998; 98US-0103840.
XX
PR 24-JUN-1998; 98US-0103840.
XX
PA (GENO-) INST GENOMIC RES.
XX
PI Fleischmann RD, White OR, Fraser CM, Venter JC;
XX WPI; 2001-647261/74.
XX
PT Evaluating strain variation of Mycobacterium tuberculosis, comprises
PT determining the nucleotide sequence of the strain at positions in the
PT genome corresponding to positions where M. tuberculosis strains CDC
PT 1551 and H37Rv differ -
XX
XX
XX Claim 4; SEQ ID NO 2; 3pp + Sequence Listing; English.
XX
XX The invention relates to evaluating strain variation within and between
CC different populations of the tuberculosis bacterial pathogen,
CC Mycobacterium tuberculosis or related Mycobacterium by determining the
CC nucleotide sequence of the first strain at positions in the complete
CC sequence of the genome that correspond to positions that differ in the
CC nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and
CC H37Rv (AA199682). The method is useful for evaluating strain variation of
CC M. tuberculosis and has valuable application in the fields of
CC tuberculosis genetics, epidemiology, patient treatment and epidemic
CC monitoring.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from USPTO
CC at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
CC
XX
XX Sequence 4403765 BP; 757105 A; 1447799 C; 1441301 G; 757371 T; 189 other;
SQ

Query Match 14.6%; Score 34.4; DB 22; Length 4403765;
Best Local Similarity 73.3%; Pred. No. 3.9;
Matches 44; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 171 gaccgcgcacatcgcgcacattgcccgtgcagacgcgcactcacctcgaagtgtgcaa 230
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Db 1567783 gaccgcgcgcctacgcgcacattcggcgcgcacgcgaagtcgaattaccgttggagcagctcga 1567842

RESULT 30
AA199682
ID AA199682 standard; DNA: 4411529 BP.
XX

```


KW cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;
KW genetic disease; haematopoietic disorder; platelet disorder; asthma;
KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;
KW allergic rhinitis; diabetes; multiple sclerosis; depression;
KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
KW neurological disorder; ss.
OS Homo sapiens.
XX
XX WO200153455-A2.
PN
XX
XX 26-JUL-2001.
PD
XX
XX 22-DEC-2000; 2000WO-US35017.
PE
XX
XX 23-DEC-1999; 99US-0471275.
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
XX
XX (HYSE-) HYSEQ INC.
PA
XX
PI Tang YT, Liu C, Drmanac RT;
DR WPI: 2001-457603/49.
DR P-PSDB; AAM25863.
XX
XX Isolated human polynucleotides encoding polypeptides, useful for the
PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
XX
XX Claim 1; Page 659; 1217pp; English.
XX
XX AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
CC AAH25963. The proteins can have activities based on the tissues and
CC cells they are expressed in, such as: antinflammatory; antirheumatic;
CC antiarthritic; immunosuppressive; antibacterial; endocrine; cardiac;
CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;
CC cardiovascular; antianaemic; antiagregant; haemostatic; vulnereary;
CC anticancer; osteopathic; dermatologic; antiallergic; antiasthmatic;
CC antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic;
CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides
CC encoding them can be used in gene therapy, antisense therapy and vaccine
CC production. The proteins and polynucleotides are useful for screening for
CC agonists or antagonists of a protein and for the treatment and diagnosis
CC of disorders associated with the activity of a protein e.g. inflammation,
CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,
CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal
CC infections, autoimmunity, genetic diseases, haematopoietic disorders,
CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,
CC osteoporosis, severe combined immunodeficiency, eczema, allergic
CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,
CC Alzheimer's disease, Parkinson's disease, neurodegenerative and
CC neurological disorders.
XX
XX Sequence 1844 BP; 444 A; 484 C; 535 G; 380 T; 1 other;
SQ

Query Match 13.38; Score 31.2; DB 22; Length 1844;
Best Local Similarity 41.08; Pred. NO. 1.7;
Matches 66; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

QY 25 agatgcacgcgcgcacatcgtataaagcgtacgtatcattgctgtgtattt 84
DB 1635 AGCGCGATGTTTAAAGGCTATCATCTGAGAGCCCTGTGACGCTTCCTTTT 1576
QY 85 aatgtctataatcagagacacacacacgtacgttannnnnnnnnnnnnnnnnn 144
DB 1575 ATGCGTTAAAAATTTGTATGTTGGGCGACGACGCGTGCCTACGCCCTGTAATCCACA 1516
QY 145 nnn 185
DB 1515 CTGGAGGCCGAGGCGGATCATGATGATGATGATGATGATGATGATGATGATG 1475

RESULT 33
AAS59515/C
ID AAS59515 standard; DNA; 66788 BP.
XX
XX AAS59515;
AC
XX
XX 13-FEB-2002 (first entry)
XX
XX Propionibacterium acnes immunogenic protein encoding DNA #10.
XX
XX
XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
KW dermatological; osteopathic; neuroprotectant; ds.
XX
XX Propionibacterium acnes.
XX
XX WO200161581-A2.
PN
XX
XX 01-NOV-2001.
PD
XX
XX 20-APR-2001; 2001WO-US12865.
PF
XX
XX 21-APR-2000; 2000US-199047P.
PR 02-JUN-2000; 2000US-208841P.
PR 07-JUL-2000; 2000US-216747P.
XX
XX (CORI-) CORIXA CORP.
PA
XX
PI Skelky YAW, Persing DH, Mitcham JL, Wang SS, Bhatia A;
PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
DR WPI: 2001-616774/71.
XX
XX Propionibacterium acnes polypeptides and nucleic acids useful for
PT vaccinating against and diagnosing infections, especially useful for
PT treating acne vulgaris -
XX
XX Claim 1; SEQ ID NO 10; 1069pp; English.
XX
XX Sequences AAS59506-AAS59804 represent DNA molecules encoding
CC Propionibacterium acnes immunogenic polypeptides. The proteins and their
CC associated DNA sequences are used in the treatment, prevention and
CC diagnosis of medical conditions caused by P. acnes. The disorders include
CC SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and
CC osteomyelitis), uveitis and endophthalmitis. P. acnes is also involved
CC in infections of bone, joints and the central nervous system, however it
CC is particularly involved in the inflammatory lesions associated with acne
CC vulgaris. A method for detecting the presence or absence of P. acnes in a
CC patient comprises contacting a sample with a binding agent that binds to
CC the proteins of the invention and determining the amount of bound protein
CC in the sample. The polypeptides may be used as antigens in the production
CC of antibodies specific for P. acnes proteins. These antibodies can be
CC used to downregulate expression and activity of P. acnes polypeptides and
CC therefore treat P. acnes infections. The antibodies may also be used as
CC diagnostic agents for determining P. acnes presence, for example, by
CC enzyme linked immunosorbent assay (ELISA). This sequence encodes the
CC polypeptides shown in AAU61313-42019 and AAU674473.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 66788 BP; 13534 A; 21369 C; 19347 G; 12530 T; 8 other;
SQ

Query Match 13.18; Score 30.8; DB 23; Length 66788;
Best Local Similarity 41.78; Pred. NO. 11;
Matches 53; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 105 gacacacacgtacgttann 164
DB 26120 GAAGCGTCGGCGAGGTTTCATTTTGGCTGGCCCTGGGCTGTGTGAAGACCGAGCT 26061

QY 165 catcaagaccgcgcacatcgcgaccttggccgtgacgacgcgcacttcacctgcagagt 224
 || ||||| | | | | | ||||| | | ||||| | | ||||| | |
 Db 26060 CACCAAGCGCGTACACGAGTTCCCTTGGGAGAGAGAGAGCCCTCATACCCCTGACAT 26001
 OY 225 ggtcaag 231
 | | | | |
 Db 26000 GAGCGAG 25994

RESULT 34
 AAS1580/C
 ID AAS1580 standard; DNA: 606 BP.
 AC AAS1580;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Pseudomonas aeruginosa DNA for cellular proliferation protein #165.
 XX
 KM Antisense; ds: prokaryotic cellular proliferation gene;
 KM antibiotic; antibacterial; drug design.
 XX
 OS Pseudomonas aeruginosa.
 XX
 PN WO200170955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 21-MAR-2001; 2001WO-US09180.
 XX
 PR 21-MAR-2000; 2000US-191078P.
 PR 23-MAY-2000; 2000US-206848P.
 PR 26-MAY-2000; 2000US-207727P.
 PR 23-OCT-2000; 2000US-242578P.
 PR 27-NOV-2000; 2000US-253625P.
 PR 22-DEC-2000; 2000US-257931P.
 PR 16-FEB-2001; 2001US-269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Hesselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX
 DR WPI; 2001-611495/70.
 DR P-PSDB; AAU33721.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics; comprise sequences of antisense nucleic acids -
 XX
 PS Claim 27; Seq ID No 4162; 511pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation. Their use in identifying the
 CC genes, their use in the discovery of novel antibiotics, the essential
 CC genes themselves and the encoded proteins. The prokaryotes used are
 CC *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella*
 CC *pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The
 CC invention is also useful for the identification of potential new targets
 CC for antibiotic development. The antisense nucleic acids can also be used
 CC to identify proteins used in proliferation, to express these proteins,
 CC and to obtain antibodies capable of binding to the expressed proteins.
 CC The proteins can be used to screen compounds in rational drug discovery
 CC programmes. The antisense nucleic acid sequence is also useful to screen
 CC for homologous nucleic acids which are required for cell proliferation in
 CC a wide variety of organisms. The present sequence encodes an
 CC essential prokaryotic cellular proliferation protein.
 CC Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic
 CC format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 606 BP; 121 A; 212 C; 185 G; 88 T; 0 other;

Query Match 13.0%; Score 30.6; DB 23; Length 606;
 Best Local Similarity 68.9%; Pred. No. 1.7;
 Matches 42; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY 174 cgcgcacatcgcgcaccttggccgtgacgacgcgcacttcacctgcagagtgcacagcc 233
 ||||| | | | | | ||||| | | ||||| | | ||||| | |
 Db 106 CGCCGCAATACCGCGCTTCCCTGCGCCCGCGGCAATCCAGCGCATGCGCAAGGC 47

OY 234 c 234
 |
 Db 46 C 46

RESULT 35
 AAF12426
 ID AAF12426 standard; cDNA: 657 BP.
 XX
 AC AAF12426;
 XX
 DT 13-MAR-2001 (first entry)
 XX
 DE *Aspergillus oryzae* EST SEQ ID NO:4949.
 XX
 KM Multiple gene expression; filamentous fungal cell; EST;
 KM expressed sequence tag; *Fusarium venenatum*; *Aspergillus niger*;
 KM *Aspergillus oryzae*; *Trichoderma reesei*; identification; recombination;
 KM culture condition; environmental stress; spore morphogenesis;
 KM metabolic pathway engineering; catabolic pathway engineering; ss.
 XX
 OS *Aspergillus oryzae*.
 XX
 PN WO200056762-A2.
 XX
 PD 28-SEP-2000.
 XX
 PF 22-MAR-2000; 2000WO-US07781.
 XX
 PR 22-MAR-1999; 99US-0273623.
 XX
 PA (NOVO) NOVO NORDISK BIOTECH INC.
 PA (NOVO) NOVO NORDISK AS.
 XX
 PI Berka RM, Rey MW, Shuster JR, Kaupinen S, Clausen IG, Olsen PB;
 PI WPI; 2000-594572/56.
 XX
 DR Monitoring differential expression of genes in filamentous fungal cells
 DR PT uses fluorescence-labeled nucleic acids isolated from the cells and a
 DR PT substrate of expressed sequence tags -
 XX
 PS Claim 88; Page 2084; 3161pp; English.
 XX
 CC The present invention describes a method for monitoring differential
 CC expression of genes in a first filamentous fungal (FF) cell relative to
 CC expression of the same genes in one or more second filamentous fungal
 CC cells. The method uses fluorescence-labeled nucleic acids isolated from
 CC the FF cells and a substrate of expressed sequence tags (EST). The ESTs
 CC are used in the methods for monitoring differential expression of genes
 CC in a first filamentous fungal (FF) cell relative to expression of the
 CC same genes in one or more second filamentous fungal cells. Monitoring
 CC the global expression of genes from FF cells allows the production
 CC potential of the microorganisms to be improved. New genes may be
 CC discovered, possible functions of unknown open reading frames can be
 CC identified and gene copy number variation and stability can be
 CC monitored. The expression of genes can be used to study how FF cells
 CC adapt to changes in culture conditions, environmental stress, spore
 CC morphogenesis, recombination, metabolic or catabolic pathway
 CC engineering. Using ESTs provides several advantages over genomic or
 CC random cDNA clones including elimination of redundancy as one spot on an
 CC array equals one gene or open reading frame, and organisation of the
 CC microarrays based on function of the gene products to facilitate
 CC analysis of the results. AAF07478 to AAF1247 represents ESTs from

the global e

XX

WPI: 1999-005

WPI: 1999-005

XX	P-PSDB;AAW81635-36.
PT	New isolated lepidoptera GABA-gated chloride channels - comprise 3 isoforms isolated from the tobacco budworm <i>Heliopsis virescens</i> , used for characterizing bioactive agents, e.g. insecticides
PS	Claim Id: Fig 2: 55pp; English.
CC	This cDNA sequence encompasses the open reading frame encoding GABA-gated chloride channel TBW-a3 (see AAW81635-36) of tobacco budworm (<i>Heliopsis virescens</i>). TBW-a3, TBW-a2 (see AAW81633-34) and TBW-a1 (see AAW81637) proteins are 3 receptor isoforms that show sequence homology to each other and to other insect GABA-gated chloride channels. TBW-2a cDNA was obtained from <i>H. virescens</i> 4th instar larva RNA by PCR and RACE amplifications. The invention provides expression vectors in which a nucleic acid encoding a GABA-gated chloride channel is driven by an inducible promoter, and a claimed process for producing a GABA-gated chloride channel by transformed cells. The GABA-gated channels or cells expressing them can be used for characterizing a bioactive agent (claimed), e.g. for use as an insecticide. Probes and primers that identify or amplify GABA-gated chloride channel nucleic acids of the invention are also claimed.
SQ	Sequence 1519 BP; 421 A; 362 C; 347 G; 388 T; 1 other;
Query Match	12.7%; Score 29.8; DB 20; Length 1519;
Best Local Similarity	40.5%; Pred. No. 4.8;
Matches	64; Conservative 0; Mismatches 94; Indels 0; Gaps 0.
OY	2 ttcttcgctcagcctcggtlgacagatgcgctggcccatgctgtaaatgtagcgtcct 61
Db	253 ttttacttcagacaatttgtagctgacctgcgattagcatataaaaaagaaccggaagt 312
OY	62 gatcatgcttcgttgtttttaatgtttatatattgatgcagagcaaacacgtaagtt 121
Db	313 gaacatttatctgtgtggcctccaattcataaagaacatatggttacccgacagcttctt 372
OY	122 nnn 159
Db	373 gtaaataagaagcaatctatttcataatagcaacaac 410
RESULT	38
ABLO09035	
ID	ABL09035 standard; CDNA: 3550 BP.
XX	AC ABL09035;
XX	DT 26-MAR-2002 (first entry)
XX	DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 21587.
XX	Drosophila; developmental biology; cell signalling; Insecticide;
KW	pharmaceutical; gene; ss.
OS	Drosophila melanogaster.
XX	WO200171042-A2.
PN	27-SEP-2001.
XX	PD 23-MAR-2001; 2001WO-US09231.
PF	23-MAR-2001; 2000US-191637P.
PR	23-MAR-2000; 2000US-191637P.
PR	11-JUL-2000; 2000US-0614150.
XX	(PEKE) PE CORP NY.
XX	Venter JC, Adams M, Li PWD, Myers EW;
PI	WPI; 2001-656860/75.
DR	

[illegible]

Sequence 1221 BP; 272 A; 350 C; 336 G; 263 T; 0 other;

[illegible]

AC AAT04566;
XX
26-APR-1996 (first entry)
DT
XX
S-adenosylmethionine synthetase DNA.
DE
XX
XX
Coryneform bacteria; S-adenosylmethionine synthetase; production; ss
KW
XX
Brevibacterium flavum strain MJ-233.
XX
XX

PA (MITU) MITSUBISHI CHEM CORP
XX
DDR WPI; 1995-331524/43.
DDR P-PSDB; AAR80060.
XX

CC The DNA encodes a S-adenosylmethionine synthetase derived from a
CC *Corynebacterium* bacterium. The DNA is used to transform bacteria to
CC efficiently produce the enzyme. A 5.5 kb SalI DNA fragment cont.
CC this DNA gives fragments of 2.4, 1.7 and 1.4 kb when cleaved with
CC BamHI and fragments of 3.3, 1.0, 0.7 and 0.5 kb when cleaved with PstI
XX
XX Sequence 1239 BP; 279 A; 347 G; 339 G; 274 T; 0 other:

[illegible]

RESULT 45

AC AAF71873;

DE Corynebacterium glutamicum MP protein nucleotide sequence SEQ ID NO:241.

KM Corynebacterium glutamicum; metabolic pathway protein; MP protein;
 KM fine chemical production; microorganism; organic acid; nucleoside;
 KM nonproteinogenic amino acid; purine base; pyrimidine base; nucleotide;
 KM lipid; saturated fatty acid; unsaturated fatty acid; diol; vitamin;
 KM carbohydrate; aromatic compound; cofactor; polypeptide; enzyme; ds.

PN WO200100843-A2

PF 23-JUN-2000; 2000WO-IB00923.

[illegible]

PR	08-JUL-1999;	99DE-1031573.
PR	08-JUL-1999;	99DE-1031592.
PR	08-JUL-1999;	99DE-1031632.
PR	08-JUL-1999;	99DE-1031634.
PR	08-JUL-1999;	99DE-1031636.
PR	09-JUL-1999;	99DE-1032125.
PR	09-JUL-1999;	99DE-1032126.
PR	09-JUL-1999;	99DE-1032130.
PR	09-JUL-1999;	99DE-1032186.
PR	09-JUL-1999;	99DE-1032206.
PR	09-JUL-1999;	99DE-1032227.
PR	09-JUL-1999;	99DE-1032228.
PR	09-JUL-1999;	99DE-1032229.
PR	09-JUL-1999;	99DE-1032230.
PR	14-JUL-1999;	99DE-1032922.
PR	14-JUL-1999;	99DE-1032926.
PR	14-JUL-1999;	99DE-1032928.
PR	14-JUL-1999;	99DE-1033004.
PR	14-JUL-1999;	99DE-1033005.
PR	14-JUL-1999;	99DE-1033006.
PR	12-AUG-1999;	99US-0146813.
PR	27-AUG-1999;	99DE-1040764.
PR	27-AUG-1999;	99DE-1040765.
PR	27-AUG-1999;	99DE-1040766.
PR	27-AUG-1999;	99DE-1040832.
PR	31-AUG-1999;	99DE-1041378.
PR	31-AUG-1999;	99DE-1041379.
PR	31-AUG-1999;	99DE-1041380.
PR	31-AUG-1999;	99DE-1041394.
PR	31-AUG-1999;	99DE-1041396.
PR	03-SEP-1999;	99DE-1042076.
PR	03-SEP-1999;	99DE-1042077.
PR	03-SEP-1999;	99DE-1042079.
PR	03-SEP-1999;	99DE-1042086.
PR	03-SEP-1999;	99DE-1042087.
PR	03-SEP-1999;	99DE-1042088.
PR	03-SEP-1999;	99DE-1042095.
PR	03-SEP-1999;	99DE-1042124.
PR	03-SEP-1999;	99DE-1042129.
PR	09-MAR-2000;	2000US-0187970.

PA (BADI) BASF AG.
 XX
 PI Pompejus M, Kroegeer B, Schroeder H, Zelder O, Habernauer G;
 XX
 DR WPI: 2001-137957/14.
 DR P-PSDS: AAB/9754.
 XX
 XX Nucleic acids from *Corynebacterium glutamicum* encoding metabolic
 PT pathway proteins, useful for producing fine chemicals in
 PT microorganisms, including organic acids, nonproteinogenic amino acids,
 PT and purine and pyrimidine bases -
 XX
 XX Claim 3; Page 507-509; 1737bp; English.
 XX
 XX AAE71753 to AAE72330 encode the *Corynebacterium glutamicum* metabolic
 CC pathway (MP) proteins given in AAB79634 to AAB80211. The C. glutamicum
 CC MP nucleic acids are useful for the production of fine chemicals
 CC in microorganisms, including organic acids, nonproteinogenic amino
 CC acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids,
 CC saturated and unsaturated fatty acids, diols, carbohydrates, aromatic
 CC compounds, vitamins, cofactors, polyketides and enzymes.
 XX
 XX Sequence 1344 BP; 306 A; 369 C; 357 G; 312 T; 0 other;

Query Match	12.3%	Score 29;	DB 22;	Length 1344;
Best Local Similarity	41.0%;	Pred. No. 8.7;		
Matches 50;	Conservative 0;	Mismatches 72;	Indels 0;	Gaps 0;

Oy 113 acgtacgcttcnntnnnnnnnnnnnnnnnnnnnnnnnnncaggttcatcaaga 172
||| ||| | | | |
Db 1167 accgcgctccagcagcaattatccgttgagcttgatctgcttcgcgatctaagctgaca 1226b

Oy	173	ccgcgcatacagccactttggccgctgagcagccgactaacctcgcaggtgtrcaagc	232
db	1227	ctctgtcctacagccactttgtgcgcacgatttgacctctctctggagagctatgcac	1286
Oy	233	cc	234
db	1287	gc	1288

Search completed: August 20, 2002, 01:47:32
Job time: 5161 sec

APPLICATION NUMBER: FR 92/114411

```

; SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:

```

FILING DATE: 25-SEP-1992

1 COUNTRY: USA
2 ZIP: 20005-3315
3
4 COMPUTER READABLE FORM:
5 MEDIUM TYPE: floppy disk
6 COMPUTER: IBM PC compatible
7 OPERATING SYSTEM: PC-DOS/MS-DOS
8 SOFTWARE: Patent In Release #1.0, Version #1.30
9 CURRENT APPLICATION DATA:
10 APPLICATION NUMBER: US/08/403,852D
11 FILING DATE: 10-MAY-1995
12
13 PRIOR APPLICATION DATA:
14 APPLICATION NUMBER: PCT/FR 93/00923
15 FILING DATE: 25-SEP-1993
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: FR 92/11441
18 FILING DATE: 25-SEP-1992
19
20 ATTORNEY/AGENT INFORMATION:
21 NAME: Meyers, Kenneth J.
22 REGISTRATION NUMBER: 25,146
23 REFERENCE/DOCKET NUMBER: 03806.0054-00000
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: (202) 408-4000
26 TELEFAX: (202) 408-4400
27
28 INFORMATION FOR SEQ ID NO: 1:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 5392 base pairs
31 TYPE: nucleic acid
32 STRANDEDNESS: double
33 TOPOLOGY: linear
34 MOLECULE TYPE: cdna
35 HYPOTHETICAL: NO
36
37

ORGANISM: *S.pistinaespiralis*
US-08-403-852D-1

Query Match	17.1%	Score 40.2	DB 2	Length 5392
Best Local Similarity	46.7%	Pred. No. 0.00024		
Matches	57	Conservative	0	Mismatches 65; Indels 0; Gaps 0;
QY	113	acgtcgcgttmmmmmmmmmmmmmmmmmmmmmmmmmmmmmmnnnnnncaggtccatcaaga	172	
DB	4612	ACCTCGGCCGCCGCCATCCGCACTTCGACCTGCTGGGCCCATCTACGCCGCCA	4671	
QY	173	ccgcgcgcatacgcgcacttgcgcgtgacgcacgcacttaacctcgcagtggtccaagc	232	
DB	4672	CCGCGCCCTACGGCCACTTCGGCCGCCGAACTCCCGACTTACCTGGGGCGCCAGCCACC	4731	

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Db      4732 GC 4733
1
RESULT      5
US-08-510-646B-1
: Sequence 1, Application US/08510646B
: Patent No. 6077699
: GENERAL INFORMATION:
: APPLICANT:  Blanc, Veronique
: APPLICANT:  Crouzet, Joel
: APPLICANT:  Jacques, Nathalie
: APPLICANT:  Lacroix, Patricia
: APPLICANT:  Thibaut, Denis
: APPLICANT:  Zagorec, Monique
: APPLICANT:  Debussche, Laurent
: APPLICANT:  De Crecy-Lagard, Valerie
: TITLE OF INVENTION:  Polypeptides Involved In The
: TITLE OF INVENTION:  Biosynthesis Of Streptogramins, Nucleotide Sequences
: TITLE OF INVENTION:  Coding For These Polypeptides And Their Use
: NUMBER OF SEQUENCES: 45
: CORRESPONDENCE ADDRESS:
:

```


	Query Match	16.8%	Score 39.4;	DB 3;	Length 1693;
	Best Local Similarity	47.3%;	Pred. No. 0.00027;		
	Matches 52;	Conservative 0;	Mismatches 58;	Indels 0;	Gaps 0;
Qy	113 acgtacgctnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncaggcttcataaga	172			
Ddb	848 acctccggcccgcgcgatcatccgcgacctcgactcgcgccgagatctactccaga	789			
Qy	173 ccggccgaacagccacattggccgtagcaagcagcacattaccitcgag	222			
Ddb	788 cggcgcccttacggccacttggcgccgcgacagctccggagctttacccttgagag	739			

```

RESULT 12
US-09-103-840A-1
, Sequence 1, Application US/09103840A
, Patent No. 6294328
, GENERAL INFORMATION:
, APPLICANT: FLEISCHMAN, Robert D.
, APPLICANT: WHITE, Owen R.
, APPLICANT: FRASER, Claire M.
, APPLICANT: VENTER, John C.
, TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
, TITLE OF INVENTION: TUBERCULOSIS
, FILE REFERENCE: 24366-20007.00
, CURRENT APPLICATION NUMBER: US/09/103,840A
, CURRENT FILING DATE: 1998-06-24
, NUMBER OF SEQ ID NOS: 2
, SOFTWARE: PatentIn Ver. 2.1
, SEQ ID NO 1
, LENGTH: 4411529
, TYPE: DNA
, ORGANISM: Mycobacterium tuberculosis
, OTHER INFORMATION: H37Rv
US-09-103-840A-1

```

```

Query Match 14.6%  Score 34.4; DB 4; Length 4411529;
Best Local Similarity 73.3%; Pred. NO. 0.55;
Matches 44; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 171 gaccgcgcgcatacagcgcacattggcgcgtgaacagccgcactcaactcgcaggtgtgcaaa 230
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Ddb 1567944 gaccgcgcgccttaacgagcacttgcgcgcgaacgcgcgtcgattaccgltggagcagcagctcga 1568003

```

Patent No. 6329516
GENERAL INFORMATION:
APPLICANT: Halling, Blaik
TITLE OF INVENTION: Lepidopteran GABA-Gated Chloride
TITLE OF INVENTION: Channels
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,361
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1519 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1..1443
OTHER INFORMATION:
US-09-002-361-4

Query Match 12.7%; Score 29.8; DB 4; Length 1519;
Best Local Similarity 40.5%; Pred. No. 0.59;
Matches 64; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

QY 2 ttccgctagcctcgtgagacagatgcgcgtgcccattgctgataaattgagcgtcct 61
DB 253 TTTTACTTACAGACATTTTGGACTGATCCTCGATTAGCATACAAAAAGACACCGAGTT 312
QY 62 gatccattgctgctgctgctatattgctgctatattgctgctgctgctgctgctgct 121
DB 313 GAAACTTATCTGCTGGGCTCAGCAATCATTAAGAACATATGCTGCTGCTGCTGCT 372
QY 122 nnn 159
DB 373 GTAATGAAAGCAATCTTATTTCATATAGCAACAAC 410

RESULT 14
US-08-804-372A-31
Sequence 31, Application US/08804372A
Patent No. 6183753
GENERAL INFORMATION:
APPLICANT: Cochran, Mark D.
APPLICANT: Wild, Martha A.
APPLICANT: Winslow, Barbara J.
TITLE OF INVENTION: Recombinant Chimeric Viruses and Uses
TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/804,372A
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 2552/39115E
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 594 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 1..594
US-08-804-372A-31

Query Match 12.6%; Score 29.6; DB 4; Length 594;
Best Local Similarity 64.7%; Pred. No. 0.45;
Matches 44; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 168 caagccgcgcacatgagcacttggcgtgagacgcccagctcacccgcgaggtcgt 227
DB 87 CACCGCTCCGCTGCGACGACCATCTGCCGCCAGAGCCACCATCTTCTGCGCAGACCT 146
QY 228 caagcccc 235
DB 147 CCAGCTCC 154

RESULT 15
US-08-139-909-1
Sequence 1, Application US/08139909
Patent No. 5641656
GENERAL INFORMATION:
APPLICANT: Sekellick, Margaret J.
TITLE OF INVENTION: CHICKEN INTERFERON GENE AND NOVEL
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

RESULT 17
 : Sequence 1, Application US/08831627
 : Patent No. 6020465
 : GENERAL INFORMATION:
 : APPLICANT: Sekellick, Margaret J.
 : APPLICANT: Marcus, Philip I.
 : APPLICANT: Ferrandino, Anthony F.
 : TITLE OF INVENTION: CHICKEN INTERFERON GENE AND NOVEL
 : TITLE OF INVENTION: RECOMBINANT DNA
 : NUMBER OF SEQUENCES: 6
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 : STREET: Two Millia Drive
 : CITY: Lexington
 : STATE: Massachusetts
 : COUNTRY: USA
 : ZIP: 02173
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.30
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 : APPLICATION NUMBER: US/08/831,627
 : FILING DATE: 09-APR-1997
 : CLASSIFICATION: 530
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 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/235,402
 : FILING DATE: 28-APR-1994
 : APPLICATION NUMBER: US 08/139,909
 : FILING DATE: 22-OCT-1993
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Carroll, Alice O.
 : REGISTRATION NUMBER: 33,542
 : REFERENCE/DOCKET NUMBER: UCT93-04A
 : TELECOMMUNICATION INFORMATION:

REFERENCE/DOCKET NUMBER: APV-036.02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 11:

MOLECULE TYPE: CDNA
US-08-136-742A-3

1224cagylccatccagaccgcgcacac 103

; Patent No. 5972995

; Patent No. 5972995


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US-08-951-912-1/C
; Sequence 1, Application US/08951912
; Patent No. 5972995
; GENERAL INFORMATION:
; APPLICANT: Fischer, Horst
; APPLICANT: Illek, Beate
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CYSTIC
; FIBROSIS THERAPY
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,912
; FILING DATE: 16-OCT-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MAKI, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 200116.403
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6129 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 133..4572
US-08-951-912-1

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Best Local Similarity 40.5%; Pred. No. 3.5;
Matches 53; Conservative 0; Mismatches 78; Indels 0; Gaps 0.

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QY      124  nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnncagltcatcaagaacgcgcataac 183
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DB      4003  GTGGATATACCTCCAAAGCGCTTCTCCTCCACTGTTGCAAAAGTTATTTGAATCCCAAGACACAC 3944

QY      184  ggcaccacttgg 194
         | | | | |
DB      3943  CATGCATCTCG 3933

RESULT 31
US-08-951-912-5/c
; Sequence 5, Application US/08951912
; Patent No. 5972995
; GENERAL INFORMATION:
; APPLICANT: Fischer, Horst
; APPLICANT: Illek, Beate
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CYSTIC
; FIBROSIS THERAPY
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:

```

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1 ADDRESSSEE: SEED and BERRY LLP
2 STREET: 6300 Columbia Center, 701 Fifth Avenue
3 CITY: Seattle
4 STATE: Washington
5 COUNTRY: USA
6 ZIP: 98104
7
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: Floppy disk
10 COMPUTER: IBM PC compatible
11 OPERATING SYSTEM: PC-DOS/MS-DOS
12 SOFTWARE: Patent Release #1.0, Version #1.30
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14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/08/951,912
16 FILING DATE: 16-OCT-1997
17 CLASSIFICATION: 514
18 ATTORNEY/AGENT INFORMATION:
19 NAME: Maki, David J.
20 REGISTRATION NUMBER: 31,392
21 REFERENCE/DOCKET NUMBER: 200116.403
22 TELECOMMUNICATION INFORMATION:
23 TELEPHONE: (206) 622-4900
24 TELEFAX: (206) 682-6031
25 INFORMATION FOR SEQ ID NO: 5:
26 SEQUENCE CHARACTERISTICS:
27 LENGTH: 6129 base pairs
28 TYPE: nucleic acid
29 STRANDEDNESS: single
30 TOPOLOGY: linear
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RESULT 33
 US-09-248-026-1/c
 ; Sequence 1, Application US/09248026
 ; Patent No. 6093567
 ; GENERAL INFORMATION:
 APPLICANT: Gregory, R.J., Armentano, D., Couture, L.A., Smith,
 APPLICANT: A.E.
 TITLE OF INVENTION: ADENOVIRUS VECTORS FOR GENE THERAPY
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: BAKER & BOTTS, L.L.P.
 STREET: 30 ROCKEFELLER PLAZA
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10112
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/248,026
 FILING DATE: 10-FEB-1999
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/895,194
 FILING DATE: 16-JUL-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Seide, Rochelle K.

RESULT 34
 US-08-681-838A-1/c
 : Sequence 1, Application US/08681838A
 : Patent No. 6245735
 : GENERAL INFORMATION:
 : APPLICANT: Pier, Gerald B
 : TITLE OF INVENTION: Methods and Products for Treating
 : TITLE OF INVENTION: Pseudomonas Infection
 : NUMBER OF SEQUENCES: 5
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Wolf, Greenfield & Sacks PC
 : STREET: 600 Atlantic Avenue
 : CITY: Boston
 : STATE: MA
 : COUNTRY: USA
 : ZIP: 02210
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentln Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/681.838A
 : FILING DATE:
 : CLASSIFICATION: 514
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Gates, Edward R
 : REGISTRATION NUMBER: 31,616
 : REFERENCE/DOCKET NUMBER: B0801/7054
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 617-720-3500
 : TELEFAX: 617-720-2441
 : INFORMATION FOR SEQ ID NO: 1:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 6129 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear

RESULT 45
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; Sequence 1, Application US/08471112A
; Patent No. 6313264
; GENERAL INFORMATION:
; APPLICANT: Molnar-Kimber, Katherine L.
; APPLICANT: Falli, Amedeo F.
; APPLICANT: Cagliano, Thomas J.

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OM nucleic - nucleic search, using sw model

Run on: August 20, 2002, 00:26:11 ; Search time 3447.21 Seconds

(without alignments)
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Title: US-09-198-779b-1

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Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	198	84.3	235	15 US-09-198-779b-1	Sequence 1, Appl
2	198	84.3	235	16 US-09-236-218A-2024	Sequence 2024, Ap
3	198	84.3	235	35 US-09-955-568-2024	Sequence 2024, Ap
4	198	84.3	242	17 US-09-304-517A-936	Sequence 936, App
5	198	84.3	242	17 US-09-371-146A-936	Sequence 936, App
6	198	84.3	242	36 US-09-985-678-936	Sequence 936, App
7	198	84.3	482	25 US-09-654-617-259077	Sequence 259077,
8	198	84.3	482	27 US-09-684-016-259077	Sequence 156999, A
9	121	51.5	368	33 US-09-865-419A-16999	Sequence 138, App
10	121	51.5	399	23 US-09-619-643-138	Sequence 8, Appl
11	121	51.5	399	53 US-60-146-907-8	Sequence 58459, A
12	121	51.5	449	59 US-60-207-458-58459	Sequence 58459, A
13	121	51.5	473	59 US-60-207-458-58453	Sequence 15364, A
14	121	51.5	502	59 US-60-207-458-15364	Sequence 9449, Ap
15	121	51.5	509	32 US-09-849-526A-9449	Sequence 9449, Ap
16	121	51.5	509	59 US-60-202-214-9449	Sequence 9449, Ap
17	121	51.5	526	33 US-09-873-402A-43368	Sequence 43368, A
18	121	51.5	526	33 US-09-865-419A-52675	Sequence 52675, A
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20	121	51.5	547	59 US-60-207-458-136690	Sequence 92612, A
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22	121	51.5	560	59 US-60-207-458-139436	Sequence 139436, A
23	121	51.5	607	33 US-09-865-439A-62153	Sequence 62153, A
24	121	51.5	607	59 US-60-207-458-106313	Sequence 106313, A
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26	121	51.5	615	59 US-60-209-830-56416	Sequence 56416, A
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ALIGNMENTS

Sequence 1, Application US/09198779HE

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Sequence 2024, Application US/09236218A

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NUMBER OF SEQ ID NOS: 3838

LENGTH: 235

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NAME/KEY: unsure

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181 taccac

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Sequence 2024

APPLICANT: H

APPLICANT: G

TITLE OF INVESTIGATION

CURRENT FILLING

NUMBER OF SEC
PRIOR FILING

SEO ID NO 2024

TYPE: DNA

FEATURE:

OTHER INFORMATION:

LOCATION: 12

US 09-006-60-50

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Db 368 t 368

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; Sequence 8, Application US/60146907
; GENERAL INFORMATION:
; APPLICANT: Fisher, Dane K.
; APPLICANT: Laigudi, Raghunath V.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(51365)A
; CURRENT APPLICATION NUMBER: US/60/146, 907
; NUMBER OF SEQ ID NOS: 3607
; SEQ ID NO 8
; LENGTH: 399
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3115-014-PI-K1-G4
US-60-146-907-8

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Db 308 tgatccattgctggtgtatataatgtatagacagacacacacgtacgt 367
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Db 368 t 368

RESULT 12
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; Sequence 58459, Application US/60207458
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Deikman, Jill
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Laigudi, Raghunath V.
; APPLICANT: Ruan, Yijun G.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Sammons, R. Douglas
; APPLICANT: Shukla, Hridayabhiranjan
; APPLICANT: Wu, Kunsheng
; APPLICANT: Xu, Nanfei
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(51936)A
; CURRENT APPLICATION NUMBER: US/60/207, 458
; NUMBER OF SEQ ID NOS: 152403
; SEQ ID NO 58459
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: uc-zmflb73012c08a2
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Best Local Similarity 100.0%; Pred. No. 7,1e-29;
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QY 61 tgatccattgctggtgtatataatgtatagacagacacacacgtacgt 120
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Db 61 tgatccattgctggtgtatataatgtatagacagacacacacgtacgt 2
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QY 121 t 121
Db 1 t 1

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; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Deikman, Jill
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Laigudi, Raghunath V.
; APPLICANT: Ruan, Yijun G.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Sammons, R. Douglas
; APPLICANT: Shukla, Hridayabhiranjan
; APPLICANT: Wu, Kunsheng
; APPLICANT: Xu, Nanfei
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
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; SEQ ID NO 58453
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: uc-zmflb73012b12a2
US-60-207-458-58453

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Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; Sequence 15364, Application US/60207458
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Deikman, Jill
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Laigudi, Raghunath V.
; APPLICANT: Ruan, Yijun G.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Sammons, R. Douglas
; APPLICANT: Shukla, Hridayabhiranjan
; APPLICANT: Wu, Kunsheng
; APPLICANT: Xu, Nanfei
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(51936)A
; CURRENT APPLICATION NUMBER: US/60/207, 458
; NUMBER OF SEQ ID NOS: 152403
; SEQ ID NO 58459
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: uc-zmflb73012c08a2
US-60-207-458-58459

RESULT 14
US-60-207-458-15364/C
; Sequence 15364, Application US/60207458
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Deikman, Jill
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Laigudi, Raghunath V.
; APPLICANT: Ruan, Yijun G.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Sammons, R. Douglas
; APPLICANT: Shukla, Hridayabhiranjan
; APPLICANT: Wu, Kunsheng
; APPLICANT: Xu, Nanfei
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(51936)A
; CURRENT APPLICATION NUMBER: US/60/207, 458
; NUMBER OF SEQ ID NOS: 152403
; SEQ ID NO 58459
; LENGTH: 449
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: uc-zmflb73012c08a2
US-60-207-458-58459

```

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ruaf, Yijun G.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Sammons, R. Douglas
; APPLICANT: Shukla, Hridayabhiranjan
; APPLICANT: Wu, Kunsheng
; APPLICANT: Xu, Nanfei
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 38-21(51936)A
; CURRENT APPLICATION NUMBER: US/60/207,458
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 152403
; SEQ ID NO 15364
; LENGTH: 502
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: uc-zmf1mo17346c10a1
US-60-207-458-15364
```

```
Query Match
Best Local Similarity 51.5%; Score 121; DB 59; Length 502;
100.0%; Pred. No. 7.4e-29;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 gtttcgctagcctcggtgacagatcgacgctgcccacgtgataatgagcgctc 60
    |||||||
Db 146 GTTTCCGCTAGCCTCGGTGACAGATCGACGCTGCCATCTGATAATGACGGTCC 87
    |||||||
Qy 61 tgatccattgttcgtgtgtatattgttataatgagagagacacagctagct 120
    |||||||
Db 86 TGATCCATTGTTCTGTGTATTATTATGTTATATTGAGACAGACACACGCTAGCT 27
    |||||||
Qy 121 t 121
    |
Db 26 T 26
```

```

RESULT 15
US-09-849-526A-9449/c
; Sequence 9449, Application US/09849526A
; GENERAL INFORMATION:
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Shukla, Hridayabhiranjan
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 16517.250(38-21(51930)B)
; CURRENT APPLICATION NUMBER: US/09/849,526A
; CURRENT FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: US 60/202,214
; PRIOR FILING DATE: 2000-05-08
; PRIOR APPLICATION NUMBER: US 09/654,617
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: US 09/684,016
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/816,660
; PRIOR FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 30131
; SEQ ID NO 9449
; LENGTH: 509
; TYPE: DNA
; ORGANISM: Zea mays subsp. mexicana
; FEATURE:
; OTHER INFORMATION: Clone ID: uc-zmroteosinte073b07a1
US-09-849-526A-9449
```

```
Query Match
Best Local Similarity 51.5%; Score 121; DB 32; Length 509;
100.0%; Pred. No. 7.4e-29;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 gtttcgctagcctcggtgacagatcgacgctgcccacgtgataatgagcgctc 60
```

```

Db 133 GTTTCCGCTAGCCTCGGTGACAGATCGACGCTGCCATCTGATAATGACCGTCC 74
    |||||||
Qy 61 tgatccattgttcgtgtgtatattgttataatgagagagacacacagctagct 120
    |||||||
Db 73 TGATCCATTGTTCTGTGTATTATTATGTTATATTGAGACAGACACACGCTAGCT 14
    |||||||
Qy 121 t 121
    |
Db 13 T 13
```

```

RESULT 16
US-60-202-214-9449/c
; Sequence 9449, Application US/60202214
; GENERAL INFORMATION:
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Shukla, Hridayabhiranjan
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 38-21(51930)A
; CURRENT APPLICATION NUMBER: US/60/202,214
; CURRENT FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 29880
; SEQ ID NO 9449
; LENGTH: 509
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: uc-zmroteosinte073b07a1
US-60-202-214-9449
```

```
Query Match
Best Local Similarity 51.5%; Score 121; DB 59; Length 509;
100.0%; Pred. No. 7.4e-29;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 gtttcgctagcctcggtgacagatcgacgctgcccacgtgataatgagcgctc 60
    |||||||
Db 133 GTTTCCGCTAGCCTCGGTGACAGATCGACGCTGCCATCTGATAATGACGGTCC 74
    |||||||
Qy 61 tgatccattgttcgtgtgtatattgttataatgagagagacacacagctagct 120
    |||||||
Db 73 TGATCCATTGTTCTGTGTATTATTATGTTATATTGAGACAGACACACGCTAGCT 14
    |||||||
Qy 121 t 121
    |
Db 13 T 13
```

```

RESULT 17
US-09-873-402A-43368/c
; Sequence 43368, Application US/09873402A
; GENERAL INFORMATION:
; APPLICANT: Edgeron, Michael D
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: Varagona, Marguerite J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51934)B
; CURRENT APPLICATION NUMBER: US/09/873,402A
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,830
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 90966
; SEQ ID NO 43368
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3595-016-Q1-N6-G8
US-09-873-402A-43368
```

```
Query Match          51.5%; Score 121; DB 33; Length 526;
Best Local Similarity 100.0%; Pred. No. 7.5e-29;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtttcgcttagcctcggtgagacagatcgacgctgccatgctgataaatgagcgtcc 60
    |||||||
Db 121 GTTTCGCTTAGCCTCGGTGAGACAGATCGACGCTGCCATGCTGATTAATGAGCGGTCC 62

QY 61 tgatccattgtcgtgtgtatataatggttataattgagcagacacacagctact 120
    |||||||
Db 61 TGATCCATTGTCGTGTGTATTAATGTTGTATTAATTGACGACGACACACAGCTACGT 2

QY 121 t 121
    |
Db 1 T 1

RESULT 18
US-09-865-419A-52142/C
; Sequence 52142, Application US/09865419A
; GENERAL INFORMATION:
; APPLICANT: Conner, Timothy W.
; APPLICANT: Wu, Kunsheng
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(51935)B
; CURRENT APPLICATION NUMBER: US/09/865,419A
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/208,063
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 54020
; SEQ ID NO 52142
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3637-241-Q6-N6-A4
US-09-865-419A-52142

Query Match          51.5%; Score 121; DB 33; Length 528;
Best Local Similarity 100.0%; Pred. No. 7.5e-29;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtttcgcttagcctcggtgagacagatcgacgctgccatgctgataaatgagcgtcc 60
    |||||||
Db 127 GTTTCGCTTAGCCTCGGTGAGACAGATCGACGCTGCCATGCTGATTAATGAGCGGTCC 68

QY 61 tgatccattgtcgtgtgtatataatggttataattgagcagacacacacagctact 120
    |||||||
Db 67 TGATCCATTGTCGTGTGTATTAATGTTGTATTAATTGACGACGACACACAGCTACGT 8

QY 121 t 121
    |
Db 7 T 7

RESULT 19
US-09-865-439A-92675/C
; Sequence 92675, Application US/09865439A
; GENERAL INFORMATION:
; APPLICANT: Edgerman, Michael D
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(51936)B
; CURRENT APPLICATION NUMBER: US/09/865,439A
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/207,458
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 119126
; SEQ ID NO 92675
```

```
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3607-012-Q6-N6-H9
US-09-865-439A-92675

Query Match          51.5%; Score 121; DB 33; Length 547;
Best Local Similarity 100.0%; Pred. No. 7.6e-29;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtttcgcttagcctcggtgagacagatcgacgctgccatgctgataaatgagcgtcc 60
    |||||||
Db 127 GTTTCGCTTAGCCTCGGTGAGACAGATCGACGCTGCCATGCTGATTAATGAGCGGTCC 68

QY 61 tgatccattgtcgtgtgtatataatggttataattgagcagacacacacagctact 120
    |||||||
Db 67 TGATCCATTGTCGTGTGTATTAATGTTGTATTAATTGACGACGACACACAGCTACGT 8

QY 121 t 121
    |
Db 7 T 7

RESULT 20
US-60-207-458-136690/C
; Sequence 136690, Application US/60207458
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Delkman, Jill
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Lalgudi, Raghuath V.
; APPLICANT: Ruan, Yijun G.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Sammons, R. Douglas
; APPLICANT: Shukla, Hridayabhiranjan
; APPLICANT: Wu, Kunsheng
; APPLICANT: Xu, Nanfei
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(51936)A
; CURRENT APPLICATION NUMBER: US/60/207,458
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 152403
; SEQ ID NO 136690
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3607-012-Q6-N6-H9
US-60-207-458-136690

Query Match          51.5%; Score 121; DB 59; Length 547;
Best Local Similarity 100.0%; Pred. No. 7.6e-29;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 gtttcgcttagcctcggtgagacagatcgacgctgccatgctgataaatgagcgtcc 60
    |||||||
Db 127 GTTTCGCTTAGCCTCGGTGAGACAGATCGACGCTGCCATGCTGATTAATGAGCGGTCC 68

QY 61 tgatccattgtcgtgtgtatataatggttataattgagcagacacacacagctact 120
    |||||||
Db 67 TGATCCATTGTCGTGTGTATTAATGTTGTATTAATTGACGACGACACACAGCTACGT 8

QY 121 t 121
    |
Db 7 T 7

RESULT 21
```

Query Match	51.58;	Score 121;	DB 59;	Length 560;
Best Local Similarity	100.08;	Pred. No. 7.6e-29;		
Matches 121; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

APPLICANT:	Adad, Mark S.
APPLICANT:	Conner, Timothy W.
APPLICANT:	Deikman, Jill
APPLICANT:	Hardeman, Kristine J.
APPLICANT:	La Rosa, Thomas J.
APPLICANT:	Lalgudi, Raghunath V.
APPLICANT:	Ruan, Yijun G.
APPLICANT:	Ruff, Thomas G.
APPLICANT:	Sammons, R. Douglas
APPLICANT:	Shukla, Hridayabhiranjan
APPLICANT:	Wu, Kunsheng
APPLICANT:	Xu, Nanfei
TITLE OF INVENTION:	NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH PLANTS


```

: FILE REFERENCE: 38-21(51936)A
: CURRENT APPLICATION NUMBER: US/60/207,458
: CURRENT FILING DATE: 2000-05-30
: NUMBER OF SEQ ID NOS: 152403
: SEQ ID NO 106313
: LENGTH: 607
: TYPE: DNA
: ORGANISM: Zea mays
: OTHER INFORMATION: Clone ID: LIB3587-218-01-N6-F8
: US-60-207-458-106313

```

Query Match	51.5%;	Score 121;	DB 59;	Length 607;
Best Local Similarity	100.0%;	Pred. No. 7.8e-29;		
Matches 121;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY 1 gtttcgcgtctagccctcggctgacagatbcagcctgcaccatcgtataatatgacggtcc 60
 |||||
Db 127 GTTTCGCTAGCCCTCGGTGCACAGATGACGCGGCCCATCTGATTAATGCACGGTCC 68

Qy	121	t	121
Db	7	r	7

```

RESULT 25
US-09-873-402A-84677/C
Sequence 84677, Application US/09873402A
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
APPLICANT: Hardeman, Kristine J.
APPLICANT: Varagona, Marguerite J.
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(51934)B
CURRENT APPLICATION NUMBER: US/09/873,402A
CURRENT FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/209,830
PRIOR FILING DATE: 2000-06-06
NUMBER OF SEQ ID NOS: 90966
SEQ ID NO 84677
LENGTH: 615
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3689-230-Q1-N6-G3
US-09-873-402A-84677

```

Query Match	51.5%	Score 121;	DB 33;	Length 615;
Best Local Similarity	100.0%	Pred. No. 7.8e-29;		
Matches 121; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Oy 1 gtcttcgctcgaagctcggatggagaagatcgacagctgcccacgtcgcgtatgaatgaagacgctc 60
 | |||||
 Db 121 GTTTCGCTAGAGCTCGGTGGAGACATCCAGCGTGGCCATGCTGATTAATGAGAGGTCC 62
 |||||
 Oy 61 tgatccattgttcgtgtgtattataaagtgtataattgacgaggaacacacacgtacgt 120
 | |||||
 Db 61 TGAATCCATGTCGTCGTGTATTATTAATGTTGTATTAATTGACAGGACACAAACGTACGT 2
 |||||
 Oy 121 t 121
 |
 Db 1 T 1

RESULT 26
US-60-209-830-56416/c
; Sequence 56416, Application US/60209830

```

: GENERAL INFORMATION:
: APPLICANT: Andersen, Scott E.
: APPLICANT: Castiglioni, Paolo
: APPLICANT: Hardeman, Kristine J.
: APPLICANT: Keek, Nancy M.
: APPLICANT: La Rosa, Thomas J.
: TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED W
: TITLE OF INVENTION: PLANTS
: FILE REFERENCE: 38-21(51934)A
: CURRENT APPLICATION NUMBER: US/60/209,830
: CURRENT FILING DATE: 2000-06-06
: NUMBER OF SEQ ID NOS: 62628
: SEQ ID NO 56416
: LENGTH: 615
: TYPE: DNA
: ORGANISM: Zea mays
: OTHER INFORMATION: Clone ID: LIB3689-230-Q1-N6-G3
: US-60-209-830-56416

```

Query Match	51.5%;	Score 121;	DB 59;	Length 615;
Best Local Similarity	100.0%;	Pred. No. 7.8e-29;		
Matches 121;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 gtttcgcgtcagccctcgctgacacatcgacgcgcccatgtcataaatgacggtcc 60
Db 121 GTTTCCGCTCAGCCCTCGGTGGACAGATGCACGCTGCCCATGCTGATAATGGACGCTCC 62

Qy 61 tgaccatcgttcgttgcgtatataaagttgataattgagcagacacacacgtacgt 120
|||||
Db 61 TGATCCATCTGTCGTTGTGTTAATTAAGTGTGTAATTCAGCAGACACACACGTACGT 2

QY	121	t	121
		—	
Db	1	T	1

```

RESULT 27
US-09-654-617-259066/c
: Sequence 259066, Application US/09654617
: GENERAL INFORMATION:
: APPLICANT: Kovalic, David K.
: APPLICANT: Liu, Jingdong
: TITLE OF INVENTION: Annotated Plant Genes
: FILE REFERENCE: 38-21(45097)D
: CURRENT APPLICATION NUMBER: US/09/654, 617
: CURRENT FILING DATE: 2000-09-05
: NUMBER OF SEQ ID NOS: 463173
: SEQ ID NO 259066
: LENGTH: 2233
: TYPE: DNA
: ORGANISM: Zea mays
US-09-654-617-259066

```

Query Match	51.5%	Score 121;	DB 25;	length 2233;
Best Local Similarity	100.0%	Pred. No. 1.2e-28;		
Matches 121;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

RESULT 28

QY 1 gtttcgcgtacgctcggtgagacagatcgacgctgccatgctgtataaattgagcgtcc 60
|||||
Db 215 GTTTCGCTAGCCTCGGTGAGACAGATCGACCGCTGCCCATGCTGATTAATGAGCGGTCC 156
QY 61 tgatccatgctcggtgtgtatataatgtgtataaattgagcagacacacagctacgt 120
|||||
Db 155 TGATCCATGTTGCTGTGTATTATGTTATGTTAATTGAGACAGACACAAACGAAACGT 96
QY 121 t 121
+
Db 95 T 95

RESULT 32

US-09-873-402A-85870/C
; Sequence 85870, Application US/09873402A
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: Varagona, Marguerite J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51934)B
; CURRENT APPLICATION NUMBER: US/09/873,402A
; CURRENT FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/209,830
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 90966
; SEQ ID NO 85870
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3689-238-Q1-N6-G5
US-09-873-402A-85870

Query Match 49.4%; Score 116; DB 33; Length 609;
Best Local Similarity 100.0%; Pred. No. 3.4e-27;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gtttcgcgtacgctcggtgagacagatcgacgctgccatgctgtataaattgagcgtcc 60
|||||
Db 116 GTTTCGCTAGCCTCGGTGAGACAGATCGACCGCTGCCCATGCTGATTAATGAGCGGTCC 57
QY 61 tgatccatgctcggtgtgtatataatgtgtataaattgagcagacacacacgt 116
|||||
Db 56 TGATCCATGTTGCTGTGTATTATGTTAATTGAGACAGACAAACGCT 1

RESULT 33

US-60-209-830-57609/C
; Sequence 57609, Application US/60209830
; GENERAL INFORMATION:
; APPLICANT: Andersen, Scott E.
; APPLICANT: Castiglioni, Paolo
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: Kerr, Nancy M.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 38-21(51934)A
; CURRENT APPLICATION NUMBER: US/60/209,830
; CURRENT FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 62628
; SEQ ID NO 57609
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3689-238-Q1-N6-G5
US-60-209-830-57609

Query Match 49.4%; Score 116; DB 59; Length 609;
Best Local Similarity 100.0%; Pred. No. 3.4e-27;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 gtttcgcgtacgctcggtgagacagatcgacgctgccatgctgtataaattgagcgtcc 60
|||||
Db 116 GTTTCGCTAGCCTCGGTGAGACAGATCGACCGCTGCCCATGCTGATTAATGAGCGGTCC 57
QY 61 tgatccatgctcggtgtgtatataatgtgtataaattgagcagacacacacgt 116
|||||
Db 56 TGATCCATGTTGCTGTGTATTATGTTAATTGAGACAGACAAACGCT 1

RESULT 34

US-09-865-439A-71349/C
; Sequence 71349, Application US/09865439A
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51936)B
; CURRENT APPLICATION NUMBER: US/09/865,439A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/207,458
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 119126
; SEQ ID NO 71349
; LENGTH: 713
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: jC-zmshLIB3587P001h03a1
US-09-865-439A-71349

Query Match 48.1%; Score 113; DB 33; Length 713;
Best Local Similarity 95.9%; Pred. No. 3.5e-26;
Matches 116; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 gtttcgcgtacgctcggtgagacagatcgacgctgccatgctgtataaattgagcgtcc 60
|||||
Db 131 GTTTCGCTAGCCTCGGTGAGACAGATCGACCGCTGCCCATGCTGATTAATGAGCGGTCC 72
QY 61 tgatccatgctcggtgtgtatataatgtgtataaattgagcagacacacacgt 120
|||||
Db 71 TGATCCATGTTGCTGTGTATTATGTTAATTGAGACAGAGACTCTACAAACGA 12
QY 121 t 121
+
Db 11 T 11

RESULT 35

US-60-207-458-115496/C
; Sequence 115496, Application US/60207458
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Deikman, Jill
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Laligudi, Raghunath V.
; APPLICANT: Ruan, Yijun G.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Sammons, R. Douglas
; APPLICANT: Spukla, Hridayabhiraanjan
; APPLICANT: Wu, Kunsheng
; APPLICANT: Xu, Nanfei
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS

```
FILE REFERENCE: 38-21(51936)A
CURRENT APPLICATION NUMBER: US/60/207,458
CURRENT FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 152403
SEQ ID NO 115496
LENGTH: 713
TYPE: DNA
ORGANISM: Zea mays
OTHER INFORMATION: Clone ID: jC-zmshLIB3587P001h03a1
US-60-207-458-115496
```

```
Query Match
Best Local Similarity 48.1%; Score 113; DB 59; Length 713;
Matches 116; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 gtttcgctcagcctcggtgagacagatcgacgctgcccattgctgataatgagcggtcc 60
DB 131 GTTTCCGCTAGCCCTGGGTGGACAGATCGACGCTGCCCATGCTGATTAATGACGCGTCC 72
QY 61 tgatccattgtcgtgtgtatataatgtgtataatgagcagagacacagcgtaagt 120
DB 71 TGATCCATGTGCTGTGTATTAATGTTGATTAATTGACGAGACTCTACACAAACA 12
QY 121 t 121
DB 11 T 11
```

```
RESULT 36
US-09-865-419A-34794/C
Sequence 34794, Application US/09865419A
GENERAL INFORMATION:
APPLICANT: Conner, Timothy W.
APPLICANT: Wu, Kunsheng
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(51935)B
CURRENT APPLICATION NUMBER: US/09/865,419A
CURRENT FILING DATE: 2001-05-29
PRIORITY FILING DATE: 2000-05-31
PRIORITY FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 54020
SEQ ID NO 34794
LENGTH: 607
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3600-034-Q6-N6-F9
US-09-865-419A-34794
```

```
Query Match
Best Local Similarity 47.7%; Score 112; DB 33; Length 607;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 gtttcgctcagcctcggtgagacagatcgacgctgcccattgctgataatgagcggtcc 60
DB 112 GTTTCCGCTAGCCCTGGGTGGACAGATCGACGCTGCCCATGCTGATTAATGACGCGTCC 53
QY 61 tgatccattgtcgtgtgtatataatgtgtataatgagcagagacacac 112
DB 52 TGATCCATGTGCTGTGTATTAATGTTGATTAATTGACGAGACACAAAC 1
```

```
RESULT 37
US-60-208-063-17853/C
Sequence 17853, Application US/60208063
GENERAL INFORMATION:
APPLICANT: Andersen, Scott E.
APPLICANT: Conner, Timothy W.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Laljundi, Raghunath V.
```

```
APPLICANT: Ruff, Thomas G.
APPLICANT: Shukla, Hridayabhiranjan
APPLICANT: Wu, Kunsheng
APPLICANT: Xu, Nanfei
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WI
FILE REFERENCE: 38-21(51935)A
CURRENT APPLICATION NUMBER: US/60/208,063
CURRENT FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 25021
SEQ ID NO 17853
LENGTH: 607
TYPE: DNA
ORGANISM: Zea mays
OTHER INFORMATION: Clone ID: LIB3600-034-Q6-N6-F9
US-60-208-063-17853
```

```
Query Match
Best Local Similarity 47.7%; Score 112; DB 59; Length 607;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 gtttcgctcagcctcggtgagacagatcgacgctgcccattgctgataatgagcggtcc 60
DB 112 GTTTCCGCTAGCCCTGGGTGGACAGATCGACGCTGCCCATGCTGATTAATGACGCGTCC 53
QY 61 tgatccattgtcgtgtgtatataatgtgtataatgagcagagacacac 112
DB 52 TGATCCATGTGCTGTGTATTAATGTTGATTAATTGACGAGACACAAAC 1
```

```
RESULT 38
US-09-865-439A-6402/C
Sequence 6402, Application US/09865439A
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D.
APPLICANT: Hardeman, Kristine J.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(51936)B
CURRENT APPLICATION NUMBER: US/09/865,439A
CURRENT FILING DATE: 2001-05-29
PRIORITY FILING DATE: 2000-05-30
PRIORITY FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 119126
SEQ ID NO 6402
LENGTH: 375
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3205-076-P1-N1-F7
US-09-865-439A-6402
```

```
Query Match
Best Local Similarity 47.4%; Score 111.4; DB 33; Length 375;
Matches 115; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
QY 1 gtttcgctcagcctcggtgagacagatcgacgctgcccattgctgataatgagcggtcc 60
DB 133 GTTTCCGCTAGCCCTGGGTGGACAGATCGACCTGCCCATGCTGATTAATGACGCGTCC 74
QY 61 tgatccattgtcgtgtgtatataatgtgtataatgagcagagacacacagcgtaagt 120
DB 73 TGATCCATGTGCTGTGTATTAATGTTGATTAATTGACGAGACACACCCCGCTCGT 14
QY 121 t 121
DB 13 T 13
```

```
RESULT 39
```

```
US-09-865-439A-105057/c
; Sequence 105057, Application US/09865439A
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51936)B
; CURRENT APPLICATION NUMBER: US/09/865,439A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/207,458
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 119126
; SEQ ID NO 105057
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3608-030-Q6-N6-F9
US-09-865-439A-105057
```

```
Query Match          47.4%; Score 111.4; DB 33; Length 494;
Best Local Similarity 95.0%; Pred. No. 1e-25;
Matches 115; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
OY 1 gtttcgctagcctcggtgagacagatcgacgtgcccatgctgataaattgacagcttc 60
Db 121 GTTTCCGCTCTAGCCCGCGGTGCGCCAGATCGACGCTGCCAGTGTGATAAATGGACGGTCC 62
OY 61 tgatccattgtcgtgtgtatataatggttataattgagcagacacacacagctacgt 120
Db 61 TGATCCATTGTCGTTGTGTATTATATGCTGTATTATTTGACGACGACCAACACGTCGCT 2
```

```
OY 121 t 121
Db 1 T 1
```

```
RESULT 40
US-60-207-458-148977/c
; Sequence 148977, Application US/60207458
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Deikman, Jill
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Laligudi, Raghunath V.
; APPLICANT: Ruan, Yijun G.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Sammons, R. Douglas
; APPLICANT: Shukla, Hridayabhiranjan
; APPLICANT: Wu, Kunsheng
; APPLICANT: Xu, Nanfei
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 38-21(51936)A
; CURRENT APPLICATION NUMBER: US/60/207,458
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 152403
; SEQ ID NO 148977
; LENGTH: 494
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: LIB3608-030-Q6-N6-F9
US-60-207-458-148977
```

```
Query Match          47.4%; Score 111.4; DB 59; Length 494;
Best Local Similarity 95.0%; Pred. No. 1e-25;
Matches 115; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
```

```
OY 1 gtttcgctagcctcggtgagacagatcgacgtgcccatgctgataaattgacagcttc 60
Db 121 GTTTCCGCTCTAGCCCGCGGTGCGCCAGATCGACGCTGCCAGTGTGATAAATGGACGGTCC 62
OY 61 tgatccattgtcgtgtgtatataatggttataattgagcagacacacacagctacgt 120
Db 61 TGATCCATTGTCGTTGTGTATTATATGCTGTATTATTTGACGACGACCAACACGTCGCT 2
```

```
OY 121 t 121
Db 1 T 1
```

```
RESULT 41
US-60-207-458-50308/c
; Sequence 50308, Application US/60207458
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Deikman, Jill
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Laligudi, Raghunath V.
; APPLICANT: Ruan, Yijun G.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Sammons, R. Douglas
; APPLICANT: Shukla, Hridayabhiranjan
; APPLICANT: Wu, Kunsheng
; APPLICANT: Xu, Nanfei
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 38-21(51936)A
; CURRENT APPLICATION NUMBER: US/60/207,458
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 152403
; SEQ ID NO 50308
; LENGTH: 459
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: uc-zmflb73301907a1
US-60-207-458-50308
```

```
Query Match          47.0%; Score 110.4; DB 59; Length 459;
Best Local Similarity 99.1%; Pred. No. 2.2e-25;
Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY 1 gtttcgctagcctcggtgagacagatcgacgtgcccatgctgataaattgacagcttc 60
Db 112 GTTTCCGCTCTAGCCCGCGGTGCGCCAGATCGACGCTGCCAGTGTGATAAATGGACGGTCC 53
OY 61 tgatccattgtcgtgtgtatataatggttataattgagcagacacacacac 112
Db 52 TGATCCATTGTCGTTGTGTATTATATGCTGTATTATTTGACGACGACCAAC 1
```

```
RESULT 42
US-09-865-439A-4731/c
; Sequence 4731, Application US/09865439A
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(51936)B
; CURRENT APPLICATION NUMBER: US/09/865,439A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/207,458
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 119126
; SEQ ID NO 4731
```

```

; LENGTH: 257
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3205-056-P1-N1-B5
US-09-865-439A-4731
```

```

Query Match          46.5%; Score 109.2; DB 33; Length 257;
Best Local Similarity 71.7%; Pred. No. 4.5e-25;
Matches 114; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
```

```

QY 1 gtttcgctagcctcgtgagacagatcgacgctgccatgctgataatgagcgctcc 60
    |||||||
DB 199 GTTTCCGCTAGCCCTCGTTGGGCAATTAACCGTCCCATGCTAATAATGACGCTCC 140
    |||||||

QY 61 tgatccatgttcgctgtgtatataatgctgataatgagcagcagcagcagcagc 120
    |||||||
DB 139 TGACCCATTGTCGTTGTGTATTAATGTAATATGACGACGACACACACGTAACGT 80
    |||||||

QY 121 tnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 159
    |
DB 79 TACCCCTGTCTGTGTGTGTGTTGCATGCGCATTTGCTCTC 41
```

```

RESULT 43
US-09-865-439A-6464/c
; Sequence 6464, Application US/09865439A
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(51936)B
; CURRENT APPLICATION NUMBER: US/09/865,439A
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: US 60/207,458
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 119126
; SEQ ID NO 6464
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3205-078-P1-N1-D11
US-09-865-439A-6464
```

```

Query Match          43.3%; Score 101.8; DB 33; Length 391;
Best Local Similarity 90.1%; Pred. No. 1.4e-22;
Matches 109; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

```

QY 1 gtttcgctagcctcgtgagacagatcgacgctgccatgctgataatgagcgctcc 60
    |||||||
DB 138 GTTTCCGCTAGCCCTCGTTGGGCAATTAACCGTCCCATGCTAATAATGACGCTCC 79
    |||||||

QY 61 tgatccatgttcgctgtgtatataatgctgataatgagcagcagcagcagcagc 120
    |||||||
DB 78 TGATCCATGTGCGTTGTGTATTAATGTAATATGACGACGACGACGACGTAAGT 19
    |||||||

QY 121 t 121
    |
DB 18 T 18
```

```

RESULT 44
US-60-207-458-42142/c
; Sequence 42142, Application US/60207458
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S.
; APPLICANT: Conner, Timothy W.
; APPLICANT: Delkman, Jill
```

```

; APPLICANT: Hardeman, Kristine J.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ruan, Yijun G.
; APPLICANT: Ruff, Thomas G.
; APPLICANT: Sammons, R. Douglas
; APPLICANT: Shukla, Hridayabhiraanjan
; APPLICANT: Wu, Kunsheng
; APPLICANT: Xu, Nanfei
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WI
; FILE REFERENCE: 38-21(51936)A
; CURRENT APPLICATION NUMBER: US/60/207,458
; CURRENT FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 152403
; LENGTH: 446
; TYPE: DNA
; ORGANISM: Zea mays
; OTHER INFORMATION: Clone ID: uc-zmflb/3065g11a1
US-60-207-458-42142
```

```

Query Match          40.8%; Score 95.8; DB 59; Length 446;
Best Local Similarity 93.5%; Pred. No. 1.4e-20;
Matches 100; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```

QY 1 gtttcgctagcctcgtgagacagatcgacgctgccatgctgataatgagcgctcc 60
    |||||||
DB 107 GTTTCCGCTAGCCCGGCTGGACAGATGACCGCTCCCATGCTAATAATGACGCTCC 48
    |||||||

QY 61 tgatccatgttcgctgtgtatataatgctgataatgagcagcagcagcagcagc 107
    |||||||
DB 47 TGACCCATTGTCGTTGTGTATTAATGTAATATGACGACGACC 1
```

```

RESULT 45
US-09-692-257A-2923
; Sequence 2923, Application US/09692257A
; GENERAL INFORMATION:
; APPLICANT: Miller, Phillip W.
; APPLICANT: Peng, Ming
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
; FILE REFERENCE: 38-21(15771)B
; CURRENT APPLICATION NUMBER: US/09/692,257A
; CURRENT FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US 60/162,747
; PRIOR FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 14882
; SEQ ID NO 2923
; LENGTH: 382
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3136-015-Q1-K1-C12
US-09-692-257A-2923
```

```

Query Match          34.8%; Score 81.8; DB 27; Length 382;
Best Local Similarity 92.5%; Pred. No. 5.2e-16;
Matches 86; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

```

QY 1 gtttcgctagcctcgtgagacagatcgacgctgccatgctgataatgagcgctcc 60
    |||||||
DB 271 gtttcgctagcctcgtgagacagatcgacgctgccatgctgataatgagcgctcc 330
    |||||||

QY 61 tgatccatgttcgctgtgtatataatgagcagcagcagcagcagcagcagcagc 93
    |||||||
DB 331 tgatccatgttcgctgtgtatataatgagcagcagcagcagcagcagcagcagc 363
    |||||||
```

Tue Aug 20 07:55:45 2002

us-09-198-779b-1.rmpm

Page 15

Search completed: August 20, 2002, 02:32:18
Job time: 7567 sec

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 20, 2002, 00:56:06 ; Search time 405.84 Seconds
(Without alignments)
1519.454 Million cell updates/sec

Title: US-09-198-779B-1

Perfect score: 235
Sequence: 1 gtttcgctacgcctcgct.....ctgcgaggtgtgtcaagcccc 235

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1681217 seqs, 1312032496 residues

Total number of hits satisfying chosen parameters: 3362434

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Pending_Patents_NA_New:*
1: /cgn2_6/pdata/2/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/pdata/2/pna/US06_NEW_COMB.seq:*
3: /cgn2_6/pdata/2/pna/US07_NEW_COMB.seq:*
4: /cgn2_6/pdata/2/pna/US08_NEW_COMB.seq:*
5: /cgn2_6/pdata/2/pna/US09_NEW_COMB.seq:*
6: /cgn2_6/pdata/2/pna/US10_NEW_COMB.seq:*
7: /cgn2_6/pdata/2/pna/US11_NEW_COMB.seq:*
8: /cgn2_6/pdata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65.8	28.0	1380	US-09-424-978B-41	Sequence 41, Appl
2	61	26.0	1353	US-09-424-978B-43	Sequence 43, Appl
3	56.8	24.2	1225	US-09-975-254-27321	Sequence 27321, A
4	56.2	23.9	1377	US-10-155-881-24594	Sequence 24594, A
5	53	22.6	1485	US-09-424-978B-38	Sequence 38, Appl
6	51.4	21.9	224	US-09-975-254-22668	Sequence 22668, A
7	51.4	21.9	272	US-09-975-254-31093	Sequence 31093, A
8	51	21.7	1582	US-09-424-978B-35	Sequence 35, Appl
9	51	21.7	2183	US-09-424-978B-37	Sequence 37, Appl
10	48.8	20.8	246	US-09-975-254-28568	Sequence 28568, A
11	48.8	20.8	259	US-09-975-254-31242	Sequence 31242, A
12	48.8	20.8	1479	US-09-424-978B-40	Sequence 40, Appl
13	48.8	20.8	1940	US-10-155-881-37534	Sequence 37534, A
14	48.2	20.5	246	US-09-975-254-980	Sequence 980, App
15	48.2	20.5	251	US-09-975-254-956	Sequence 956, App
16	48.2	20.5	258	US-09-975-254-26838	Sequence 26838, A
17	46.2	19.7	257	US-09-975-254-14222	Sequence 14222, A
18	46.2	19.7	257	US-09-975-254-14222	Sequence 14222, A
19	41.6	17.5	252	US-09-975-254-30561	Sequence 30561, A
20	41.2	17.5	252	US-09-975-254-30198	Sequence 30198, A
21	39.4	16.8	1131	US-09-975-254-43077	Sequence 43077, A
22	39.4	16.8	262	US-09-975-254-28759	Sequence 28759, A
23	36.4	15.5	1188	US-60-360-039-31882	Sequence 31882, A
24	35.6	15.1	1176	US-60-360-039-35882	Sequence 35882, A
25	35.2	15.0	1149	US-60-360-039-32434	Sequence 32434, A
				US-60-360-039-28208	Sequence 28208, A

26	35.2	15.0	1149	US-60-360-039-30967	Sequence 30967, A
27	32.8	14.0	1188	US-60-360-039-26739	Sequence 26739, A
28	32	13.6	1206	US-60-360-039-39115	Sequence 39115, A
29	32	13.6	1209	US-60-360-039-39483	Sequence 39483, A
30	32	13.6	1209	US-60-360-039-39485	Sequence 39485, A
31	31.6	13.4	1203	US-60-360-039-46946	Sequence 46946, A
32	30.6	13.0	1158	US-60-360-039-44755	Sequence 44755, A
33	30.6	13.0	1161	US-60-360-039-43393	Sequence 43393, A
34	30.6	13.0	3540	US-60-360-039-33893	Sequence 33893, A
35	30	12.8	159	US-09-975-254-15822	Sequence 15822, A
36	30	12.8	1137	US-60-360-039-33823	Sequence 33823, A
37	29.8	12.7	1200	US-60-360-039-41097	Sequence 41097, A
38	29.6	12.6	625	US-60-391-781-329	Sequence 329, App
39	29.4	12.5	466	US-10-027-632-24696	Sequence 24696, A
40	29.2	12.4	548	US-10-027-632-226044	Sequence 226044, A
41	29.2	12.4	650	US-10-027-632-215532	Sequence 215532, A
42	29.2	12.4	650	US-10-027-632-215533	Sequence 215533, A
43	28.8	12.3	1001	US-60-360-039-33332	Sequence 33332, A
44	28.6	12.2	405	US-09-785-276A-48473	Sequence 48473, A
45	28.6	12.2	1764	US-60-360-039-39655	Sequence 39655, A

ALIGNMENTS

RESULT 1
US-09-424-978B-41
Sequence 41, Application US/09424978B
GENERAL INFORMATION:
APPLICANT: Falco, Saverio Carl
APPLICANT: Allen, Stephen M.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Hiltz, William D.
APPLICANT: Kinney, Anthony J.
APPLICANT: Abell, Lynne N.
APPLICANT: Thorpe, Catherine J.
TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
FILE REFERENCE: BB-1087
CURRENT APPLICATION NUMBER: US/09/424,978B
CURRENT FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: US 60/048,771
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.1
SEQ ID NO 41
LENGTH: 1380
TYPE: DNA
ORGANISM: Trillium aestiva
US-09-424-978B-41

Query Match 28.0% Score 65.8; DB 5; Length 1380;
Best Local Similarity 90.9%; Pred. No. 1,1e-12;
Matches 70; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 159 caggttcatacaagcccgcatagcgcacttggccgtgacagccgacttccactg 218
|||||
Db 1155 caggttcatacaagcccgcatagcgcacttggccgtgacagccgacttccactg 1214
QY 219 cgaagtggtcaagcccc 235
|||||
Db 1215 ggaagtggtggaagcccc 1231

RESULT 2
US-09-424-978B-43
Sequence 43, Application US/09424978B
GENERAL INFORMATION:
APPLICANT: Falco, Saverio Carl
APPLICANT: Allen, Stephen M.
APPLICANT: Rafalski, J. Antoni
APPLICANT: Hiltz, William D.
APPLICANT: Kinney, Anthony J.


```
RESULT 6
US-09-975-254-22668
; Sequence 22668, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15309)B
; CURRENT APPLICATION NUMBER: US/09/975,254
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 22668
; LENGTH: 234
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700961368H1
US-09-975-254-22668
```

```
Query Match
Best Local Similarity 21.9%; Score 51.4; DB 5; Length 234;
Matches 61; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
```

```
QY 159 caggttcatcaagaccgcgcatacgttgccgctgacgacgcgcacttcacctg 218
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 143 caggtcttgaaagactgcatacgttgcaaccttgcagagatgaccttcacatg 202
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
```

```
QY 219 cgaagtgtgtcaagccc 235
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
```

```
Db 203 ggaagtgtgtgaagccac 219
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
```

```
RESULT 7
US-09-975-254-31093
; Sequence 31093, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15309)B
; CURRENT APPLICATION NUMBER: US/09/975,254
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 31093
; LENGTH: 272
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700902279H1
US-09-975-254-31093
```

```
Query Match
Best Local Similarity 21.9%; Score 51.4; DB 5; Length 272;
Matches 61; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
```

```
QY 159 caggttcatcaagaccgcgcatacgttgccgctgacgacgcgcacttcacctg 218
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 170 caggtcttgaaagactgcatacgttgcaaccttgcagagatgaccttcacatg 229
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
```

```
QY 219 cgaagtgtgtcaagccc 235
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
```

```
Db 230 ggaagtgtgtgaagccac 246
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
```

```
RESULT 8
US-09-424-978b-35
; Sequence 35, Application US/09424978B
; GENERAL INFORMATION:
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Allen, Stephen M.
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Abell, Lynne N.
; APPLICANT: Thorpe, Catherine J.
; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
; FILE REFERENCE: BB-1087
; CURRENT APPLICATION NUMBER: US/09/424,978B
; CURRENT FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: US 60/048,771
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 1582
; TYPE: DNA
; ORGANISM: Zea mays
US-09-424-978b-35
```

```
Query Match
Best Local Similarity 21.7%; Score 51; DB 5; Length 1582;
Matches 60; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
```

```
QY 161 ggttcataaagaccgcgcatacgttgccgctgacgacgcgcacttcacctg 220
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 1230 gctacctcaagacgcgcatacgttgccgctgacgacgcgcacttcaccttcacctg 1289
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
```

```
QY 221 aggtgtgtcaagccc 235
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
```

```
Db 1290 aggtgtgtgaagccac 1304
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
```

```
RESULT 9
US-09-424-978b-37
; Sequence 37, Application US/09424978B
; GENERAL INFORMATION:
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Allen, Stephen M.
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Abell, Lynne N.
; APPLICANT: Thorpe, Catherine J.
; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
; FILE REFERENCE: BB-1087
; CURRENT APPLICATION NUMBER: US/09/424,978B
; CURRENT FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: US 60/048,771
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 2183
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-424-978b-37
```

```
Query Match
Best Local Similarity 21.7%; Score 51; DB 5; Length 2183;
Matches 60; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
```

```
QY 161 ggttcataaagaccgcgcatacgttgccgctgacgacgcgcacttcacctg 220
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db 1878 gctacctcaagacgcgcatacgttgccgctgacgacgcgcacttcaccttcacctg 1937
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
```

QY 221 aggtgtgtaagcccc 235
|||||
Db 1938 aggtgtgtaagcccc 1952

RESULT 10
US-09-975-254-28588
; Sequence 28588, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(15309)B
; CURRENT APPLICATION NUMBER: US/09/975,254
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 28588
; LENGTH: 246
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700898670H1
US-09-975-254-28588

Query Match 20.8%; Score 48.8; DB 5; Length 246;
Best Local Similarity 77.6%; Pred. No. 5, 6e-07;
Matches 59; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 160 aggtcatcaagacggcgcatagcgcaacttggccgtggaagcgagcgaacttaactgc 219
|||||
Db 9 aggtctctcaagacggcgcatagcgcaacttggcaaggaagcgaacttaactgc 68
QY 220 gaggtgtcaagcccc 235
|||||
Db 69 gaggtgtgaagccac 84

RESULT 11
US-09-975-254-31242
; Sequence 31242, Application US/09975254
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Heck, Gregory R.
; APPLICANT: La Rosa, Thomas J.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(15309)B
; CURRENT APPLICATION NUMBER: US/09/975,254
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: US/09/263,191
; PRIOR FILING DATE: 1999-03-05
; NUMBER OF SEQ ID NOS: 31255
; SEQ ID NO 31242
; LENGTH: 259
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: 700902482H1
US-09-975-254-31242

Query Match 20.8%; Score 48.8; DB 5; Length 259;
Best Local Similarity 75.7%; Pred. No. 5, 7e-07;
Matches 56; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 159 caggtcatcaagacggcgcatagcgcaacttggccgtggaagcgagcgaacttaactgc 218
|||||
Db 142 caggtctctgaagacggcgcatagcgcaacttggcaganaatgacccgaacttaactgc 201

QY 219 cgaggtgtgtaagc 232
|||||
Db 202 ggaantgtgtaagc 215

RESULT 12
US-09-424-978B-40
; Sequence 40, Application US/09424978B
; GENERAL INFORMATION:
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Allen, Stephen M.
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Hitz, William D.
; APPLICANT: Kinney, Anthony J.
; APPLICANT: Abell, Lynne N.
; TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
; FILE REFERENCE: BB-1087
; CURRENT APPLICATION NUMBER: US/09/424,978B
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: US 60/048,771
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 1479
; TYPE: DNA
; ORGANISM: Lycopersicon esculentum
US-09-424-978B-40

Query Match 20.8%; Score 48.8; DB 5; Length 1479;
Best Local Similarity 77.6%; Pred. No. 9, 9e-07;
Matches 59; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 160 aggtcatcaagacggcgcatagcgcaacttggccgtggaagcgagcgaacttaactgc 219
|||||
Db 1200 aggtctctgaagacggcgcatagcgcaacttggcaaggaagcgaacttaactgc 1259
QY 220 gaggtgtcaagcccc 235
|||||
Db 1260 gaggtgtcaagcccc 1275

RESULT 13
US-10-155-881-37534
; Sequence 37534, Application US/10155881
; GENERAL INFORMATION:
; APPLICANT: Dotson, Stanton B.
; APPLICANT: Kovalic, David K.
; APPLICANT: Liu, Jindong
; APPLICANT: Lutfiyya, Linda L.
; APPLICANT: McIninch, James
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE REFERENCE: 38-21(13500)J
; CURRENT APPLICATION NUMBER: US/10/155,881
; PRIOR FILING DATE: 2002-05-22
; NUMBER OF SEQ ID NOS: 37595
; SEQ ID NO 37534
; LENGTH: 1940
; TYPE: DNA
; ORGANISM: Glycine max
US-10-155-881-37534

Query Match 20.8%; Score 48.8; DB 7; Length 1940;
Best Local Similarity 77.6%; Pred. No. 1, 1e-06;
Matches 59; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 160 aggtcatcaagacggcgcatagcgcaacttggccgtggaagcgagcgaacttaactgc 219
|||||
Db 1614 aggtctctcaagacggcgcatagcgcaacttggcaaggaagcgaacttaactgc 1673

[illegible]

Query Match	17.7%	Score 41.6;	DB 5;	Length 252;
Best Local Similarity	76.1%;	Pred. No. 0.00018;		
Matches	50;	Conservative	0;	Indels 14;
				Gaps 0;
OY	160	aggtcatcaagacagccgcatacgcgcacttggcgtgacagcgcgacttaactgc	219	
Db	189	aggtctctcaagacagcgcgtctatgtagacacttggaaaggatgaccccttaacttaactg	248	
OY	220	gagg	223	

Query Match	16.8%	Score 39.4	DB 5	Length 262
Best Local Similarity	76.9%	Pred. No. 0.0011		
Matches 60	Conservative 0	Mismatches 17	Indels 1	Gaps 1
159	caggttcatcaagacgcgcgcata-cagcacaattgacgcgtgaagacgcgcgaattcaacct	217		
184	caggttctctgaagacgcgtgcataatggacacatttggcagagatctatnancctgttcaacct	243		


```

RESULT 30
US-60-360-039-39865
: Sequence 39865, Application US/60360039
: GENERAL INFORMATION:
: APPLICANT: Cao, Yongwei
: APPLICANT: Chen, Xianteng
: APPLICANT: Goldman, Barry S.
: APPLICANT: Hinkle, Gregory J.
: APPLICANT: Slater, Steven C.
: TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
: TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

```



```

? NUMBER OF SEQ ID NOS: 47374
? SEQ ID NO 44755
? LENGTH: 1158
? TYPE: DNA
? ORGANISM: SYNECHOCOCCUS SP. WH 8102
US-60-360-039-44755

Query Match              13.0%; Score 30.6; DB 8; Length 1158;
Best Local Similarity    73.6%; Pred. No. 2;
Matches 39; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY      170 agaccgcgacatagccacttggccgttagcagcgccgactctgaagg 222
        ||| ||||| ||||| ||||| || | ||| ||| | | ||| |||
Db       1106 acacagcgacctagcgccacttcgtctgaagcaaccttaagcccttg 1158

RESULT 33
US-60-360-039-43390
Sequence 43390, Application US/60360039
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 43390
LENGTH: 1161
TYPE: DNA
ORGANISM: Nitrosomonas europaea
US-60-360-039-43390

Query Match              13.0%; Score 30.6; DB 8; Length 1161;
Best Local Similarity    42.5%; Pred. No. 2;
Matches 45; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY      116 tacgtlnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 175
        |||||
Db       1013 taagcctcgggcccatcattcacgaactgatctgctgcgattatgcaaaacg 1072

QY      176 ccgatacgccactttggccgtgacgacgccaactctactctga 221
        ||||| ||| ||| ||||| || || || ||||| ||
Db       1073 ctgcctatgcatcttgcgcgggaagaaccacagtcttacctyga 1118

RESULT 34
US-60-360-039-33893
Sequence 33893, Application US/60360039
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Chen, Xianfeng
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)A
CURRENT APPLICATION NUMBER: US/60/360,039
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 33893
LENGTH: 3540
TYPE: DNA
ORGANISM: Cytophaga hutchinsonii
US-60-360-039-33893
```

1
2
3
4
5

```

Oy      46 ataaatgacgcgttcagt-ccattgtcctgtgttataatgttgtataattgagcg 104
         ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      131 AAAACGGAGCGTCTGTATCCCTTGTCGTTGTTGTAATTAAATGTTAATGAAGCAG 72
Oy      105 gacacaacacgt 116
         ||| |||| |
Db      71 GACCCACAGCGT 60

RESULT 39
US-10-027-632-246996
; Sequence 246996, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 246996
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-246996

Query Match          12.5%; Score 29.4; DB 7; Length 496;
Best Local Similarity 58.6%; Pred. No. 4.1;
Matches 51; Conservative 0; Mismatches 36; Indels 0; Gaps 0.

Oy      20 tggacagatcgacgctgcccatcgtcataaatgacgglcctgatcacattgttgctg 79
         ||| ||||| ||| ||| ||| ||||| ||| ||| ||| |||||
Db      24 tggcgaagtgcacctctgtgtgtgtgatatacttaacagaagaatgcgtgcagttgt 83
Oy      80 ttattaatgtgtataattgagcagga 106
         ||||| ||| ||| ||| |||
Db      84 ttatttaattgcaaaagaggaggca 110

RESULT 40
US-10-027-632-226044/c
; Sequence 226044, Application US/10027632
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
```

[illegible]

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OM of: US-09-198-779b-1 to: PIR_71.* out_format : pfs
Date: Aug 20, 2002 2:58 AM
About: Results were produced by the Gencore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame+np.model -DEV=tlp
-Q=/gen2_1/USPTO.spool/US09198779/runat.19082002.140912.2510/app.query.fasta.1.296
-DB=PIR_71 -OFMT=fastan -SUFFIX=pr -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPEL=0.000 -LOOPEXT=0.000 -OGAPOP=4.500
-OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blsum62 -TRANS=human4.0.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0
-ALIGN=45 -MODE=LOCAL -OUTFMT=pfs -NORMEXT -HEAPEXT=500
-MINLEN=0 -MAXLEN=200000000 -USER=US09198779.@CGML_1_62
-NCPU=6 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
-NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-198-779b-1
Query length: 235
Database: PIR_71.*
Database sequences: 283138
Database length: 96089334
Search time (sec): 33.210000

score_list:
Sequence Strd Orig ZScore EScore Len Documentation
PIR2:T06180 + 127.00 320.35 2.4e-10 394 methionine adenosyltransferase
PIR2:P00817 + 120.00 315.63 2.5e-09 68 methionine adenosyltransferase
PIR2:J00131 + 120.00 301.31 2.8e-09 393 methionine adenosyltransferase
PIR2:S38875 + 120.00 301.31 2.8e-09 393 methionine adenosyltransferase
PIR2:S46538 + 120.00 301.31 2.8e-09 393 methionine adenosyltransferase
PIR2:C66155 + 120.00 301.31 2.8e-09 393 methionine adenosyltransferase
PIR2:T06592 + 116.00 291.14 1.1e-08 360 methionine adenosyltransferase
PIR2:S66351 + 116.00 291.01 1.1e-08 360 methionine adenosyltransferase
PIR2:S64785 + 115.00 287.77 1.6e-08 390 probable s-adenosylmethionine s
PIR2:J00410 + 115.00 287.70 1.6e-08 393 methionine adenosyltransferase
PIR2:S66352 + 108.50 269.93 1.5e-07 397 methionine adenosyltransferase
PIR2:T07899 + 101.00 256.02 2.0e-06 179 methionine adenosyltransferase
PIR2:S49491 + 101.00 249.66 2.1e-06 390 methionine adenosyltransferase
PIR2:S46540 + 101.00 249.66 2.1e-06 390 methionine adenosyltransferase
PIR2:T10710 + 98.00 241.37 6.0e-06 396 methionine adenosyltransferase
PIR2:G72228 + 74.00 176.07 0.0260 395 s-adenosylmethionine synthetase
PIR2:EB1986 + 72.00 170.75 0.0522 389 probable methionine adenosyltr
PIR2:DB1042 + 72.00 170.75 0.0522 389 s-adenosylmethionine synthetase
PIR2:SS1671 + 68.00 159.88 0.2107 388 methionine adenosyltransferase
PIR2:DB9657 + 65.00 151.47 0.6014 400 methionine adenosyltransferase
PIR2:BB7255 + 64.50 149.96 0.7166 407 s-adenosylmethionine synthetase
PIR2:AB2895 + 64.00 149.25 0.8501 376 s-adenosylmethionine synthetase
PIR2:JW0059 + 63.50 134.33 1.09 1979 mtrp protein - mouse
PIR2:S72257 + 63.00 146.13 1.21 395 methionine adenosyltransferase
PIR2:A37118 + 63.00 145.96 1.21 395 methionine adenosyltransferase
PIR2:HB6976 + 63.00 145.96 1.21 403 probable s-adenosylmethionine s
PIR2:G67485 + 63.00 142.82 1.23 589 hypothetical protein CC1908 [lm
PIR2:P90599 + 61.00 141.08 2.42 376 hypothetical protein MYPU_7020
PIR2:D71964 + 61.00 140.89 2.43 385 s-adenosylmethionine synthetase
PIR2:EB4544 + 61.00 140.89 2.43 385 methionine adenosyltransferase
PIR2:PB9964 + 61.00 140.82 2.43 398 s-adenosylmethionine synthetase
PIR2:DB4062 + 61.00 140.60 2.43 399 s-adenosylmethionine synthetase
PIR2:PB6862 + 61.00 140.60 2.43 399 methionine adenosyltransferase
PIR2:AD1654 + 61.00 140.60 2.43 399 s-methionine adenosyltransferase
PIR2:AH1282 + 61.00 140.52 2.43 399 probable metk protein - Mycobac
PIR2:FT0899 + 61.00 140.52 2.43 403 methionine adenosyltransferase
PIR2:PB97403 + 61.00 140.18 2.44 420 s-adenosylmethionine synthetase
PIR2:AB2621 + 61.00 140.18 2.44 420 s-adenosylmethionine synthetase
PIR2:AC2211 + 61.00 134.17 2.52 877 heme transport protein alr3242
PIR2:S74736 + 60.50 139.04 2.90 409 methionine adenosyltransferase

PIR2:EB2319 + 60.00 138.17 3.44 385 s-adenosylmethionine syntha
PIR2:BB4381 - 60.00 133.60 3.53 674 acylaminoacyl-peptidase [lm
PIR2:A71281 + 59.00 135.22 4.88 396 probable s-adenosylmethionit
PIR2:A47151 + 59.00 135.22 4.88 396 methionine adenosyltransfer
PIR2:S06114 + 59.00 135.20 4.88 397 methionine adenosyltransfer

seq_name: PIR2:T06180

seq_documentation_block:

methionine adenosyltransferase (EC 2.5.1.6) - barley
N:Alternate names: S-adenosylmethionine synthetase
C:Species: Hordeum vulgare (barley)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 20-Jun-2000
C:Accession: T06180
R:Mori, S
submitted to the EMBL Data Library, August 1995
A:Reference number: Z15512
A:Accession: T06180
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-394 <MOR>
A:Cross-references: EMBL:D63835; PIDN:BA09895.1
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

alignment_scores:

Quality: 127.00 Length: 25
Ratio: 5.292 Gaps: 0
Percent Similarity: 96.000 Percent Identity: 96.000

alignment_block:

US-09-198-779b-1 x T06180 ..

Align seg 1/1 to: T06180 from: 1 to: 394

160 AGGTTTCATCAGACCGCGCATACGCGCACTTGCGCGTGACGACCGCA 209

|||||
362 ArgPheIleIleIleThrAlaAlaIleTgIhnsPheGlyAtcGAspAspAlaAs 378

210 CTTTACCTGCGAGCGTGCTCAAGCC 234

|||||
378 PPherThrTrpGluValValLysPro 386

seq_name: PIR2:P00817

seq_documentation_block:

methionine adenosyltransferase (EC 2.5.1.6) - rape (fragment)
C:Species: Brassica napus (rape)
C>Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 05-May-2000
C:Accession: P00817
R:Park, Y.S.; Kwak, J.M.; Kwon, O.Y.; Kim, Y.S.; Lee, D.S.; Cho, M.J.; Lee, H.H.; Nam
Plant Physiol. 103, 359-370, 1993
A:Title: Generation of expressed sequence tags of random root cDNA clones of Brassica
A:Reference number: P00816; MUID:94302145
A:Accession: P00817
A:Molecule type: mRNA
A:Residues: 1-68 <PAR>
A:Experimental source: root, cv. Naeahan
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

alignment_scores:

Quality: 120.00 Length: 25
Ratio: 5.217 Gaps: 0
Percent Similarity: 92.000 Percent Identity: 88.000

alignment_block:

US-09-198-779b-1 x P00817 ..

Align seg 1/1 to: P00817 from: 1 to: 68

160 AGTTTCATCAAGACCGCGCATACGGCCACTTTGGCCGTGACGACGCCGA 209
 |||||||:||||||||||||||||||||||||||||||||||||||| 11
 36 ArgpHeuLeuYstHrAlaAlaTyGlyHisPheGlyArgAspAspProAs 52
 210 CTTACACCTGCGAGGTGTCAAGCCC 234
 ||||||| |||||||
 52 pPheHrTrpGluValVallyPro 60

seq_name: p1r2:JN0131

seq_documentation_block:

methionine adenosyltransferase (EC 2.5.1.6) - Arabidopsis thaliana
 N:Alternate names: S-adenosylmethionine synthetase
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 05-May-2000
 C:Accession: JN0131
 R:Peleman, J.; Boerjan, W.; Engler, G.; Seurinck, J.; Botterman, J.; Alliotte, T.; Van M
 Plant Cell 1, 81-93, 1989
 A:Title: Strong cellular preference in the expression of a housekeeping gene of Arabidop
 A:Reference number: JN0131; MUID:92386056
 A:Accession: JN0131
 A:Molecule type: DNA
 A:Residues: 1393 <PEL>
 A:Cross-references: GB:M55077; NID:g166871; PIDN:AAA3286.1; PID:g166872
 A:Experimental source: var. K85
 A:Note: the sequence derived from var. Columbia differs from that shown in having 117-Gl
 C:Comment: S-adenosylmethionine synthetase catalyzes the biosynthesis of adenosylmethio
 C:Genetics:
 A:Gene: sam-1
 C:Superfamily: methionine adenosyltransferase
 C:Keywords: S-adenosylmethionine; transferase

alignment_scores:
 Quality: 120.00 Length: 25
 Ratio: 5.217 Gaps: 0
 Percent Similarity: 92.000 Percent Identity: 88.000

alignment_block:
 US-09-198-779B-1 x JN0131 ..

Align seg 1/1 to: JN0131 from: 1 to: 393

160 AGTTTCATCAAGACCGCGCATACGGCCACTTTGGCCGTGACGACGCCGA 209
 |||||||:||||||||||||||||||||||||||||||||||||||| 11
 361 ArgpHeuLeuYstHrAlaAlaTyGlyHisPheGlyArgAspAspProAs 377
 210 CTTACACCTGCGAGGTGTCAAGCCC 234
 ||||||| |||||||
 377 pPheHrTrpGluValVallyPro 385

seq_name: p1r2:S38875

seq_documentation_block:

methionine adenosyltransferase (EC 2.5.1.6) - tomato
 N:Alternate names: S-adenosyl-L-methionine synthetase
 C:Species: Lycopersicon esculentum (tomato)
 C>Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
 C:Accession: S46539; S38875
 R:Espartero, J.; Pintor-Toro, J.A.; Pardo, J.M.
 Plant Mol. Biol. 25, 217-227, 1994
 A:Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in res
 A:Reference number: S46538; MUID:94289646
 A:Accession: S46539
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1393 <ES2>
 A:Cross-references: EMBL:Z24742; NID:g429105; PIDN:CAA8086.1; PID:g429106
 C:Superfamily: methionine adenosyltransferase
 C:Keywords: S-adenosylmethionine; transferase

alignment_scores:
 Quality: 120.00 Length: 25
 Ratio: 5.217 Gaps: 0
 Percent Similarity: 92.000 Percent Identity: 88.000

alignment_block:
 US-09-198-779B-1 x S38875 ..

Align seg 1/1 to: S38875 from: 1 to: 393

160 AGTTTCATCAAGACCGCGCATACGGCCACTTTGGCCGTGACGACGCCGA 209
 |||||||:||||||||||||||||||||||||||||||||||||||| 11
 361 ArgpHeuLeuYstHrAlaAlaTyGlyHisPheGlyArgAspAspProAs 377
 210 CTTACACCTGCGAGGTGTCAAGCCC 234
 ||||||| |||||||
 377 pPheHrTrpGluValVallyPro 385

seq_name: p1r2:S46538

seq_documentation_block:

methionine adenosyltransferase (EC 2.5.1.6) - tomato
 N:Alternate names: S-adenosyl-L-methionine synthetase
 C:Species: Lycopersicon esculentum (tomato)
 C>Date: 26-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
 C:Accession: S46538; S38874
 R:Espartero, J.; Pintor-Toro, J.A.; Pardo, J.M.
 Plant Mol. Biol. 25, 217-227, 1994
 A:Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in
 A:Reference number: S46538; MUID:94289646
 A:Accession: S46538
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1393 <ESP>
 A:Cross-references: EMBL:Z24741; NID:g429103; PIDN:CAA8086.1; PID:g429104
 C:Superfamily: methionine adenosyltransferase
 C:Keywords: S-adenosylmethionine; transferase

alignment_scores:
 Quality: 120.00 Length: 25
 Ratio: 5.217 Gaps: 0
 Percent Similarity: 92.000 Percent Identity: 88.000

alignment_block:
 US-09-198-779B-1 x S46538 ..

Align seg 1/1 to: S46538 from: 1 to: 393

160 AGTTTCATCAAGACCGCGCATACGGCCACTTTGGCCGTGACGACGCCGA 209
 |||||||:||||||||||||||||||||||||||||||||||||||| 11
 361 ArgpHeuLeuYstHrAlaAlaTyGlyHisPheGlyArgAspAspProAs 377
 210 CTTACACCTGCGAGGTGTCAAGCCC 234
 ||||||| |||||||
 377 pPheHrTrpGluValVallyPro 385

seq_name: p1r2:C86155

seq_documentation_block:

S-adenosylmethionine synthetase [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: C86155
 R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 Nute 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marzia
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallo
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.


```

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: AB6141; MUID:21016719
A:Accession: C68155
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-393 <STO>
A:Cross-references: GB:AE005172; NID:g9972389; PIDN:AA610639.1; GSPDB:GN001414
C:Genetics:
A:Map position: 1
C:Superfamily: methionine adenosyltransferase

alignment_scores:
    Quality: 120.00      Length: 25
    Ratio: 5.217         Gaps: 0
    Percent Similarity: 92.000      Percent Identity: 88.000

alignment_block:
US-09-198-779B-1 x C68155      ..

Align seg 1/1 to: C68155 from: 1 to: 393

160 AGGTCATCATAGAGCCGCCGATACGGCCATTGGCCGTGACAGAGCCGA 209
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
361 ArgPheLeuIysThrAlaIatryIcIyIstPheGlyArgAspAspProAs 377

210 CTTGACCTGCAGGTGTCAGGCC 234
|||||  |||||||||||
377 pethertrpgIuValValysPro 385

seq_name: p1r2:T06592

seq_documentation_block:
methionine adenosyltransferase (EC 2.5.1.6) - garden pea (fragment)
C:Species: Pisum sativum (garden pea)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-May-2000
C:Accession: T06592
R:Gomez, L.; Carrasco, P.
submitted to the EMBL Data Library, January 1995
A:Description: Hormonal regulation of the S-adenosylmethionine synthase in pea
A:Reference number: 215782
A:Accession: T06592
A>Status: preliminary; translated from GB/EMBL/DBD1
A:Molecule type: mRNA
A:Residues: 1-360 <GOM>
A:Cross-references: EMBL:L36680; NID:g609556; PIDN:AA58772.1; PID:g609557
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

alignment_scores:
    Quality: 116.00      Length: 25
    Ratio: 5.043         Gaps: 0
    Percent Similarity: 92.000      Percent Identity: 84.000

alignment_block:
US-09-198-779B-1 x T06592      ..

Align seg 1/1 to: T06592 from: 1 to: 360

160 AGGTCATCATAGAGCCGCCGATACGGCCATTGGCCGTGACAGAGCCGA 209
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
330 ArgPheLeuIysThrAlaIatryIcIyIstPheGlyArgGluAspProAs 346

210 CTTGACCTGCAGGTGTCAGGCC 234
|||||  |||||||||||
346 pPethertrpgIuValValysPro 354

seq_name: p1r2:S66351

seq_documentation_block:
methionine adenosyltransferase (EC 2.5.1.6) 1 - garden pea (fragment)
C:Species: Pisum sativum (garden pea)

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C:Date: 28-Oct1996 #sequence_revision 13-Mar-1997 #text_change 05-May-2000
C:Accession: S66351
R:Gomez-Gomez, L.; Carrasco, P.
Plant Mol. Biol. 30, 821-832, 1996
A:title: Hormonal regulation of S-adenosylmethionine synthase transcripts in pea ovar
A:Reference number: S66351; MUID:96194463
A:Accession: S66351
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-366 <GOM>
A:Cross-references: EMBL:X82076; NID:9609222; PIDN:CAA57580.1; PID:9609223
A>Note: the authors did not translate the codon for residue 1
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

alignment_scores:
    Quality: 116.00      Length: 25
    Ratio: 5.043        Gaps: 0
    Percent Similarity: 92.000      Percent Identity: 84.000

alignment_block:
US-09-198-779B-1 x S66351 ..

Align seg 1/1 to: S66351 from: 1 to: 366

160 AGTTCATCATGAGACCGCCGCATATGCGCCACTTTGGCCGTGACGACGCCGA 209
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
336 ATGPhelLeuLyStThrAlaIaLyrgLHisPheGLyArgGLuAspProAs 352
210 CTTTCACCTGCGAGAGTGTCACGCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
352 pPheThrTrpGLuValIaLyAspPro 360

seq_name: p1r2:G84785

seq_documentation_block:
Probable S-adenosylmethionine synthetase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: G84785
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
A:title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: AB4420; MUID:20083487
A:Accession: G84785
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-390 <STO>
A:Cross-references: GB:AE002093; NID:94863604; PIDN:AMD31573.1; GSPDB:GN00139
A:Gene: At2g36880
A:Map position: 2
C:Superfamily: methionine adenosyltransferase

alignment_scores:
    Quality: 115.00      Length: 25
    Ratio: 5.227        Gaps: 0
    Percent Similarity: 88.000      Percent Identity: 88.000

alignment_block:
US-09-198-779B-1 x G84785 ..

Align seg 1/1 to: G84785 from: 1 to: 390

160 AGTTCATCATGAGACCGCCGCATATGCGCCACTTTGGCCGTGACGACGCCGA 209
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
361 ATGPhelLeuLyStThrAlaIaLyrgLHisPheGLyArgGLuAspProAs 377
210 CTTTCACCTGCGAGAGTGTCACGCC 234

```

|||||
377 pphenhrtrpgluvalvalyspro 385
seq_name: p1r2:JQ0410

seq_documentation_block:
methionine adenosyltransferase (EC 2.5.1.6) 2 - Arabidopsis thaliana
N:Alternate names: S-adenosylmethionine synthetase
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 05-May-2000
C:Accession: JQ0410
R:Peteman, J.; Salto, K.; Collyn, B.; Engler, G.; Seurinck, J.; Van Montagu, M.; Inze, D.
Gene 84, 359-369, 1989
A:Title: Structure and expression analyses of the S-adenosylmethionine synthetase gene
A:Reference number: JQ0410; MUID:90128280
A:Accession: JQ0410
A:Molecule type: DNA
A:Residues: 1-393 <PEL>
A:Cross-references: GB:M33217; NID:g166873; PIDN:AAA32869.1; PID:g166874
C:Genetics:
A:Gene: sam-2
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

alignment_scores:
Quality: 115.00 Length: 25
Ratio: 5.227 Gaps: 0
Percent Similarity: 88.000 Percent Identity: 88.000

alignment_block:
US-09-198-779B-1 x JQ0410 ..

Align seg 1/1 to: JQ0410 from: 1 to: 393

160 AGGTCATCAAGACCGCCGATACGGCCACTTTGGCCGTGACGACGCCGA 209
|||||
361 ArgpneGlnLysThrAlaAlaTyrGlnHisPheGlyArgAspAspProAs 377
210 CTTCACTGCGAGGTGTCAGGCC 234
|||||
377 pphenhrtrpgluvalvalyspro 385

seq_name: p1r2:S66352

seq_documentation_block:
methionine adenosyltransferase (EC 2.5.1.6) 2 - garden pea
C:Species: Pisum sativum (garden pea)
C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-May-2000
C:Accession: S66352; S52218
R:Gomez-Gomez, L.; Carrasco, P.
Plant Mol. Biol. 30, 821-832, 1996
A:Title: Hormonal regulation of S-adenosylmethionine synthase transcripts in pea ovaries
A:Reference number: S66351; MUID:96194463
A:Accession: S66352
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-397 <GOM>
A:Cross-references: EMBL:X82077
R:Gomez, L.; Carrasco, P.
Submitted to the EMBL Data Library, October 1994
A:Description: Hormonal regulation of the S-adenosylmethionine synthase in pea ovaries.
A:Reference number: S52218
A:Accession: S52218
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-364, 'FEDSCITFW' <GOM>
A:Cross-references: EMBL:X82077; NID:g609224; PIDN:CAA57581.1; PID:g609225
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

alignment_scores:

Quality: 108.50 Length: 26
Ratio: 4.717 Gaps: 1
Percent Similarity: 88.462 Percent Identity: 84.615

alignment_block:
US-09-198-779B-1 x S66352 ..

Align seg 1/1 to: S66352 from: 1 to: 397

160 AGGTC...ATCAAGACCGCCGATACGGCCACTTTGGCCGTGACGACGC 206
|||||
363 ArgpneGlnLysThrAlaAlaTyrGlnHisPheGlyArgAspAspProAs 379
207 CGACTTCACCTCGCAGGTGTCAGGCC 234
|||||
379 aasphenhrtrpgluvalvalyspro 388

seq_name: p1r2:T07899

seq_documentation_block:
methionine adenosyltransferase (EC 2.5.1.6) - Chlamydomonas reinhardtii (fragment)
N:Alternate names: S-adenosylmethionine synthetase
C:Species: Chlamydomonas reinhardtii
C>Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 05-May-2000
C:Accession: T07899
R:Kim, J.Y.; Lee, K.O.; Lee, S.H.
Submitted to the EMBL Data Library, June 1997
A:Description: Chlamydomonas reinhardtii mRNA for S-adenosylmethionine synthetase.
A:Reference number: Z16198
A:Accession: T07899
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-179 <KIM>
A:Cross-references: EMBL:AF008566; NID:g2454483; PIDN:AAB71833.1; PID:g2454484
A:Experimental source: strain 137C
C:Genetics:
A:Gene: SAMS
C:Function:
A:Description: catalyzes the formation of S-adenosyl methionine with phosphate and py
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

alignment_scores:
Quality: 101.00 Length: 24
Ratio: 4.810 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 79.167

alignment_block:
US-09-198-779B-1 x T07899 ..

Align seg 1/1 to: T07899 from: 1 to: 179

160 AGGTCATCAAGACCGCCGATACGGCCACTTTGGCCGTGACGACGCCGA 209
|||||
153 ArgTyrGlnLysThrAlaAlaTyrGlnHisPheGlyArgAspAspProAs 169
210 CTTCACTGCGAGGTGTCAG 231
|||||
169 pphenhrtrpgluvalvalys 176

seq_name: p1r2:S49491

seq_documentation_block:
methionine adenosyltransferase (EC 2.5.1.6) - garden petunia
C:Species: Petunia x hybrida (garden petunia)
C>Date: 01-Feb-1995 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
C:Accession: S49491
R:Izihaki, A.; Shoseyov, O.; Weiss, D.
Submitted to the EMBL Data Library, October 1994
A:Description: Petunia cDNA encoding S-Adenosylmethionine synthetase.
A:Reference number: S49491
A:Accession: S49491

A: Molecule type: mRNA
A: Residues: 1-390 <I2H>
A: Cross-references: EMBL:X82214; NID:g5559505; PIDN:CAA57696.1; PID:g5559506
C: Superfamily: methionine adenosyltransferase
C: Keywords: S-adenosylmethionine; transferase

alignment_scores:
Quality: 101.00 Length: 24
Ratio: 4.810 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 79.167

alignment_block:
US-09-198-779B-1 x S49491 ..

Align seg 1/1 to: S49491 from: 1 to: 390

```
160 AGGTTGATCAAGACCGCGCATACGGCCATTGGCGGTGACGACGCCGA 209
||||| ||||||| ||||||| ||||||| ||||||| ||
361 ArgTyrGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAs 377
210 CTTACCTGCGAGGTGTCAG 231
||||| ||||||| ||||||| ||||||| ||
377 pPheThrTrpGluThrValLys 384
```

seq_name: pir2:S46540

seq_documentation_block:
methionine adenosyltransferase (EC 2.5.1.6) - tomato
N: Alternate names: S-adenosyl-L-methionine synthetase
C: Species: Lycopersicon esculentum (tomato)
C: Date: 26-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
R: Accession: S46540; S38876
R: Espartero, J.; Pintor-Toro, J.A.; Pardo, J.M.
Plant Mol. Biol. 25, 217-227, 1994
A: Title: Differential accumulation of S-adenosylmethionine synthetase transcripts in res
A: Reference number: S46538; MUID:94289646
A: Accession: S46540
A: Status: nucleic acid sequence not shown
A: Molecule type: mRNA
A: Residues: 1-390 <ESP>
A: Cross-references: EMBL:Z24743; NID:g429107; PIDN:CAA80867.1; PID:g429108
C: Superfamily: methionine adenosyltransferase
C: Keywords: S-adenosylmethionine; transferase

alignment_scores:
Quality: 101.00 Length: 24
Ratio: 4.810 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 79.167

alignment_block:
US-09-198-779B-1 x S46540 ..

Align seg 1/1 to: S46540 from: 1 to: 390

```
160 AGGTTGATCAAGACCGCGCATACGGCCATTGGCGGTGACGACGCCGA 209
||||| ||||||| ||||||| ||||||| ||||||| ||
361 ArgTyrGlnLysThrAlaAlaTyrGlyHisPheGlyArgAspAspProAs 377
210 CTTACCTGCGAGGTGTCAG 231
||||| ||||||| ||||||| ||||||| ||
377 pPheThrTrpGluThrValLys 384
```

seq_name: pir2:T10710

seq_documentation_block:
methionine adenosyltransferase (EC 2.5.1.6) - clove pink
N: Alternate names: S-adenosylmethionine synthetase
C: Species: Dianthus caryophyllus (clove pink)
C: Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 05-May-2000
C: Accession: T10710
R: Larsen, P.B.; Woodson, W.R.

submitted to the EMBL Data Library, April 1991
A: Description: Cloning and nucleotide sequence of a S-adenosylmethionine synthetase
A: Reference number: Z17091
A: Accession: T10710

A: Status: translated from GB/EMBL/DBJ
A: Molecule type: mRNA
A: Residues: 1-396 <LAR>
A: Cross-references: EMBL:M61882; NID:g167961; PID:g304637
C: Genetics:
A: Gene: SAM2
C: Function:

A: Description: catalyzes the formation of S-adenosyl methionine with phosphate and p
C: Superfamily: methionine adenosyltransferase
C: Keywords: S-adenosylmethionine; transferase

alignment_scores:
Quality: 98.00 Length: 24
Ratio: 4.455 Gaps: 0
Percent Similarity: 91.667 Percent Identity: 70.833

alignment_block:
US-09-198-779B-1 x T10710 ..

Align seg 1/1 to: T10710 from: 1 to: 396

```
160 AGGTTGATCAAGACCGCGCATACGGCCATTGGCGGTGACGACGCCGA 209
||||| ||||||| ||||||| ||||||| ||||||| ||
364 ArgTyrLeuLysThrAlaAlaTyrGlyHisPheGlyArgGluAspProAs 380
210 CTTACCTGCGAGGTGTCAG 231
||||| ||||||| ||||||| ||||||| ||
380 pPheThrTrpGluAlaAlaLys 387
```

seq_name: pir2:G72228

seq_documentation_block:
S-adenosylmethionine synthetase - Thermotoga maritima (strain MSB8)
C: Species: Thermotoga maritima
C: Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C: Accession: G72228
R: Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwin, M.L.; Dodson, R.V.; Haft, D.H.; Hli
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
C.M.

Nature 399, 323-329, 1999
A: Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A: Reference number: A72200; MUID:99287316
A: Accession: G72228
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-395 <ARN>
A: Cross-references: GB:AE001807; GB:AE000512; NID:g4982216; PIDN:ABD36725.1; PID:g49.
A: Experimental source: strain MSB8
C: Genetics:
A: Gene: TM1658
C: Superfamily: methionine adenosyltransferase

alignment_scores:
Quality: 74.00 Length: 18
Ratio: 4.625 Gaps: 0
Percent Similarity: 88.889 Percent Identity: 72.222

alignment_block:
US-09-198-779B-1 x G72228 ..

Align seg 1/1 to: G72228 from: 1 to: 395

```
169 AAGACGGCGCATACGGCCATTGGCGGTGACGACGCCGACTACGCG 218
||||| ||||||| ||||||| ||||||| ||||||| ||
364 LysThrAlaAlaTyrGlyHisPheGlyArgAsnGluGluThrThr 380
219 CGAG 222
```

```

111
380 pglu 381

seq_name: p1r2:E81986

seq_documentation_block:
probable methionine adenosyltransferase (EC 2.5.1.6) NMA0663 [Imported] - Neisseria men
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C:Accession: E81986
R:Parhill, J.; Achman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis z2491.
A:Reference number: A81775; MUID:2022556
A:Accession: E81986
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-389 <PAR>
A:Cross-references: GB:AL162753; GB:AL157959; NID:97379120; PIDN:CAB83950.1; PID:9737939
A:Experimental source: serogroup A, strain z2491
C:Genetics:
A:Gene: metK: NMA0663
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

alignment_scores:
Quality: 72.00 Length: 20
Ratio: 4.235 Gaps: 0
Percent Similarity: 85.000 Percent Identity: 60.000

alignment_block:
US-09-198-779b-1 x E81986 ..

Align seg 1/1 to: E81986 from: 1 to: 389

163 TTTCATCAAGACCGCCGATACGCCACTTGGCCGTGACGACGCCGACTT 212
::: |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
356 TysSerLysSerAlaAlaTyrGlyHisPheGlyArgGluGluProGluP 372
213 CACCTGCGAG 222
|||::: |||
372 ethrTyrGlu 375

seq_name: p1r2:D81042

seq_documentation_block:
S-adenosylmethionine synthetase NMB1799 [Imported] - Neisseria meningitidis (strain MC58
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: D81042
R:Tetelin, H.; Saunders, N.J.; Heideberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.R.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Hil, H.; Qiu, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizze, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappunli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175735
A:Accession: D81042
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-389 <RET>
A:Cross-references: GB:AE002530; GB:AE002098; NID:97227054; PIDN:AAF42136.1; PID:9722705
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB1799
C:Superfamily: methionine adenosyltransferase

alignment_scores:
Quality: 72.00 Length: 20
Ratio: 4.235 Gaps: 0
```

```

Percent Similarity: 85.000 Percent Identity: 60.000

alignment_block:
US-09-198-779b-1 x D81042 ..

Align seg 1/1 to: D81042 from: 1 to: 389

163 TTTCATCAAGACCGCCGATACGCCACTTGGCCGTGACGACGCCGACTT 212
::: |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
356 TysSerLysSerAlaAlaTyrGlyHisPheGlyArgGluGluProGluP 372
213 CACCTGCGAG 222
|||::: |||
372 ethrTyrGlu 375

seq_name: p1r2:S51671

seq_documentation_block:
methionine adenosyltransferase (EC 2.5.1.6) - Acanthamoeba castellanii
C:Species: Acanthamoeba castellanii
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 05-May-2000
C:Accession: S51671
R:Ahm, K.S.; Henney, H.
submitted to the EMBL Data Library, May 1994
A:Reference number: S51671
A:Accession: S51671
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-388 <AHN>
A:Cross-references: EMBL:X79205
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

alignment_scores:
Quality: 68.00 Length: 21
Ratio: 4.250 Gaps: 0
Percent Similarity: 76.190 Percent Identity: 61.905

alignment_block:
US-09-198-779b-1 x S51671 ..

Align seg 1/1 to: S51671 from: 1 to: 388

169 AAGACCGCCGATACGCCACTTGGCCGTGACGACGCCGACTTACCTG 218
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
364 LysThrAlaTyrHisGlyHisPheGlyArgGluGluProGluPheLeu 380
219 CGAGTGTGTGACG 231
|||||::: |||
380 pgluAlaProLys 384

seq_name: p1r2:D69657

seq_documentation_block:
methionine adenosyltransferase (EC 2.5.1.6) - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000
C:Accession: D69657
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Brox, S.; Brouillet, S.; Bruschi, C.V.; Calowell, B.; Capuano, V.; Carter, N.M.;
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holtsappel, S.; Hosono, S.; Hullo, M
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A:Authors: lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y, M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scani
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terstra, P.; Tojima, A.; Tosato, V.; Uchiya
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
```


alignment_scores:

Quality: 63.50 Length: 82
Ratio: 1.411 Gaps: 2
Percent Similarity: 54.878 Percent Identity: 24.390

alignment_block:

US-09-198-779B-1/rev x JW0059 ..

Align seg 1/1 to: JW0059 from: 1 to: 1979

```

228 GACCACCTCGCAGTGAAGTCGCGCTGTCGACGCCAAAGCGCGTATG 179
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1382 AsphismetlaserglutthnglnlleuqluaspthrleuglyValcy 1398
178 C.....GGCGGTCTTCATGAC 162
1398 sValatgserGlnGlyserAlaalaaspAlaaspproAlaleuSerGluP 1415
161 CTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNAACGTACGTC 112
1415 rogluGlyasnserGluHisSerGlyserSeraspSer..... 1427
111 TTGTGCTCTGCTCAATATATACATTAATACACACACATGATG 62
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1428 LeuTrrgluAlaserleuGluasnValSerGlyThrThrAspAlaProAl 1444
61 AGACCGCTCATTTATTCAGCAGCGCAGCGTCGTCACCGA 16
|||||:|||||:|||||:|||||:|||||:|||||:
1444 aaAlaProSerValAlaIleGlnValSerValSerMetValHisGln 1459
seq_name: p1r1:S27257

```

seq_documentation_block:

methionine adenosyltransferase (EC 2.5.1.6) 2 alpha chain - human
N:Alternate names: renal methionine adenosyltransferase (MAT); S-adenosylmethionine synt
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 11-Jun-1999
C:Accession: S27257
R:Horikawa, S.; Tsukada, K.
FEBS Lett. 312, 37-41, 1992
A:Title: Molecular cloning and developmental expression of a human kidney S-adenosylmeth
A:Reference number: S27257; MUID:93050159
A:Accession: S27257
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-395 <HOR>
A:Cross-references: EMBL:X68836; GB:S47859; NID:936326; PIDN:CAA48726.1; PID:936327
C:Genetics:
A:Gene: GDB:MAT2A; SAMS2; MATA2
A:Cross-references: GDB:136213; OMIM:601468
A:Map position: 2p11.2-2p11.2
A:Introns: 15/2; 256/3
C:Complex: heterodimer of catalytic alpha and regulatory beta chains
C:Function:
A:Description: catalyzes the formation of S-adenosyl methionine with phosphate and pyroP
A:Pathway: one-carbon metabolism
C:Superfamily: methionine adenosyltransferase
C:Keywords: ATP; heterodimer; kidney; magnesium; metalloprotein; one-carbon metabolism;
F:219-286/Region: nucleotide-binding motif A (P-loop) #status atypical
F:31/Binding site: magnesium 2 (Asp) #status predicted
F:285,289/Active site: Lys #status predicted
F:291/Binding site: magnesium 1 (Asp) #status predicted

alignment_scores:

Quality: 63.00 Length: 21
Ratio: 3.938 Gaps: 1
Percent Similarity: 76.190 Percent Identity: 66.667

alignment_block:

US-09-198-779B-1 x S27257 ..

Align seg 1/1 to: S27257 from: 1 to: 395

```

169 AAGACCCGCGCATACGCGCATTGGCCGTGACGACGCCGACTTCACCTG 218
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
373 ArgThrAlaAlaTyrGlyHisPheGlyArgAsp.....SerPheProTr 387
219 CGAGGTGTCACAG 231
|||||:|||||:
387 pGluValProLys 391
seq_name: p1r2:A37118

```

seq_documentation_block:

methionine adenosyltransferase (EC 2.5.1.6) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 05-May-2000
C:Accession: A37118
R:Horikawa, S.; Sasuga, J.; Shimizu, K.; Ozasa, H.; Tsukada, K.
J. Biol. Chem. 265, 13683-13686, 1990
A:Title: Molecular cloning and nucleotide sequence of cDNA encoding the rat kidney S-
A:Reference number: A37118; MUID:90337979
A:Accession: A37118
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-395 <HOR>
A:Cross-references: GB:J05571; NID:9206845; PIDN:AAA42106.1; PID:9206846
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

alignment_scores:

Quality: 63.00 Length: 21
Ratio: 3.938 Gaps: 1
Percent Similarity: 76.190 Percent Identity: 66.667

alignment_block:

US-09-198-779B-1 x A37118 ..

Align seg 1/1 to: A37118 from: 1 to: 395

```

169 AAGACCCGCGCATACGCGCATTGGCCGTGACGACGCCGACTTCACCTG 218
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
373 ArgThrAlaAlaTyrGlyHisPheGlyArgAsp.....SerPheProTr 387
219 CGAGGTGTCACAG 231
|||||:|||||:
387 pGluValProLys 391
seq_name: p1r2:H86976

```

seq_documentation_block:

probable S-adenosylmethionine synthase [imported] - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: H86976
R:Cole, S.T.; Elgimeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.;
R.; Davies, R.M.; Devlin, K.; Dutboy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holto
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A:Authors: Rutherford, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.;
A:Title: Massive gene decay in the leprosy bacillus.
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: H86976
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-403 <STO>
A:Cross-references: GB:AL450380; NID:913092748; PIDN:CAC30052.1; GSPDN:GBN00147
C:Genetics:
A:Gene: mekK
C:Superfamily: methionine adenosyltransferase

alignment_scores:
Quality: 63.00 Length: 20
Ratio: 3.938 Gaps: 0
Percent Similarity: 80.000 Percent Identity: 55.000

alignment_block:
US-09-198-779B-1 x H86976 ..

Align seg 1/1 to: H86976 from: 1 to: 403

153 TTCATCAAGACCGCCGATAGCGCATTGGCCGTGACGACCGGACTT 212
::: |||||
372 TTTAAAGTCTTAAATATATATATATATATATATATATATATATAT 388
213 CACCTGCGAG 222
::: |||
388 UPOTPTPTPT 391

seq_name: p1r2:G87485

seq_documentation_block:

hypothetical protein CC1908 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: G87485

R:Nieman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; Debay, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolot

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: G87485

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-589 <SNO>

A:Cross-references: GB:AE005673; NID:g13423359; PIDN:AAK23883.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC1908

alignment_scores:
Quality: 63.00 Length: 61
Ratio: 1.909 Gaps: 2
Percent Similarity: 54.098 Percent Identity: 31.148

alignment_block:
US-09-198-779B-1 x G87485 ..

Align seg 1/1 to: G87485 from: 1 to: 589

53 GACGGCTCCATGATCATGTTGTTGTTATATATATATATATATGAGC 102
|||||
240 ASPLGLPTDASPPTD.....G1 245
103 AGGACACACACGTACGTTNNNNNNNNNNNNNNNNNNNNNNNNNNNN 152
||| |||||
245 nglpromeethrhisglnalaargalalasnclyserseiserSeraIag 262
153 NNNNNNAGGTTTCATCAAGACCGCCGATACGCGACATTGGCGCTGAGC 202
::: |||||
262 lylAlametalaserse...ProProAlaGlnserfargleuAlaAlasp 277
203 AGCGGACTTCACCTGCGAGGTGCTCAAGCCG 235
::: |||||
278 AlaProAspAlaProAlaAlaThrsersePro 288

seq_name: p1r2:F90599

seq_documentation_block:

hypothetical protein MYPU_7020 [imported] - Mycoplasma pulmonis (strain UAB CTIP)

C:Species: Mycoplasma pulmonis

C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001

C:Accession: F90599

R:Chambaud, I.; Hellig, R.; Ferris, S.; Barde, V.; Samson, D.; Gallsen, F.; Moszer, Nucleic Acids Res. 29, 2145-2153, 2001

A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma

A:Reference number: A9512; MUID:21267165; PMID:11353084

A:Accession: F90599

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-376 <RUR>

A:Cross-references: GB:AL445566; PID:g14090117; PIDN:CAC13875.1; GSPDB:GN00153

A:Experimental source: strain UAB CTIP

C:Genetics:

A:Gene: MYPU_7020

A:Genetic code: SGC3

C:Superfamily: methionine adenosyltransferase

alignment_scores:
Quality: 61.00 Length: 21
Ratio: 3.812 Gaps: 0
Percent Similarity: 76.190 Percent Identity: 47.619

alignment_block:
US-09-198-779B-1 x F90599 ..

Align seg 1/1 to: F90599 from: 1 to: 376

160 AGTTCATCAAGACCGCCGATACGCGCATTGGCGCGAGACCGCA 209
::: |||||
343 lylTTPheProThrSerPhePheGlyHisPheGlyArgAspPleuAs 359
210 CTTACCTGCGAG 222
::: |||
359 PleuProTPTPT 363

seq_name: p1r2:D71964

seq_documentation_block:

s-adenosylmethionine synthetase - Helicobacter pylori (strain J99)

C:Species: Helicobacter pylori

A:Variety: strain J99

C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 18-Jun-1999

C:Accession: D71964

R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Dolg, P.C.; Smith, D

ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.

Nature 397, 176-180, 1999

A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric

A:Reference number: A71800; MUID:99120557

A:Accession: D71964

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-385 <ARN>

A:Cross-references: GB:AE001456; GB:AE001439; NID:g154689; PIDN:AAD05755.1; PID:g41

A:Experimental source: strain J99

C:Genetics:

A:Gene: metK

C:Superfamily: methionine adenosyltransferase

alignment_scores:
Quality: 61.00 Length: 17
Ratio: 4.357 Gaps: 0
Percent Similarity: 82.353 Percent Identity: 64.706

alignment_block:
US-09-198-779B-1 x D71964 ..

Align seg 1/1 to: D71964 from: 1 to: 385

172 ACCGCGCATACGCGCATTGGCGGTGACGACCGGACTTCACCTGCGCA 221
||| |||||
355 ThrSerAlaTyrGlyHisPheGlyArgGluGluGluThrPheThrPseI 371
222 G 222

371 u 371

seq_name: p1r2:E64544

seq_documentation_block:
 methionine adenosyltransferase (EC 2.5.1.6) 2 - Helicobacter pylori (strain 26695)
 C:Species: Helicobacter pylori
 C>Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 05-May-2000
 C:Accession: E64544
 R:Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.
 A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: A64520; MUID:97394467
 A:Accession: E64544
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-385 <TOM>
 A:Cross-references: GB:AE000540; GB:AE000511; NID:g2313287; PIDN:AA07267.1; PID:g231328
 C:Superfamily: methionine adenosyltransferase
 C:Keywords: S-adenosylmethionine; transferase

alignment_scores:

Quality:	61.00	Length:	17
Ratio:	4.357	Gaps:	0
Percent Similarity:	82.353	Percent Identity:	64.706

alignment_block:

US-09-198-779b-1 x E64544 ..

Align seg 1/1 to: E64544 from: 1 to: 385

```

172 ACCGCCGATACGCCACTTTGGCCGTGACGACCGCAGCTTCACCTGCA 221
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
355 TnSerAlaTyrClgYHSPheGlyArgGluLeuGluGlnPheThrTrpGl 371
222 G 222
371 u 371

```

seq_name: p1r2:F89964

seq_documentation_block:
 S-adenosylmethionine synthetase [Imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: F89964
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Oi, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: F89964
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-398 <KUR>
 A:Cross-references: GB:BA000018; PID:g13701583; PIDN:BA042876.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: metK
 C:Superfamily: methionine adenosyltransferase

alignment_scores:

Quality:	61.00	Length:	18
Ratio:	4.357	Gaps:	0
Percent Similarity:	77.778	Percent Identity:	66.667

alignment_block:
 US-09-198-779b-1 x F89964 ..

Align seg 1/1 to: F89964 from: 1 to: 398

```

169 AAGACCGCCGATACGCCACTTTGGCCGTGACGACCGCAGCTTCACCTG 218
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
367 GlnThrAlaIaTyrClgYHSPheGlyArgThrAspValLeuPheProTr 383
219 CGAG 222
|||
383 pGlu 384

```

seq_name: p1r2:D84062

seq_documentation_block:
 S-adenosylmethionine synthetase metK [Imported] - Bacillus halodurans (strain C-125)
 C:Species: Bacillus halodurans
 C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
 C:Accession: D84062
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
 A:Reference number: A83650; MUID:20512582; PMID:11058132
 A:Accession: D84062
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-399 <STO>
 A:Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BA07019.1; GSPDB:G
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: metK
 C:Superfamily: methionine adenosyltransferase

alignment_scores:

Quality:	61.00	Length:	18
Ratio:	4.067	Gaps:	0
Percent Similarity:	83.333	Percent Identity:	61.111

alignment_block:

US-09-198-779b-1 x D84062 ..

Align seg 1/1 to: D84062 from: 1 to: 399

```

169 AAGACCGCCGATACGCCACTTTGGCCGTGACGACCGCAGCTTCACCTG 218
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
370 GlnThrAlaIaTyrClgYHSPheGlyArgThrAspValGluLeuProTr 386
219 CGAG 222
|||
386 pGlu 387

```

seq_name: p1r2:F86862

seq_documentation_block:
 methionine adenosyltransferase (EC 2.5.1.6) [Imported] - Lactococcus lactis subsp. Ia
 N:Alternate names: S-adenosylmethionine synthetase
 C:Species: Lactococcus lactis subsp. lactis
 C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 C:Accession: F86862
 R:Boletín, A.; Wincker, P.; Mager, S.; Jallón, O.; Malarre, K.; Weissenbach, J.; Eh Genome Res. 11, 731-753, 2001
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis
 A:Reference number: A86625; MUID:21235186; PMID:11337471
 A:Accession: F86862
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-399 <STO>
 A:Cross-references: GB:AE005176; PID:g12724937; PIDN:AA06000.1; GSPDB:GN00146
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: metK

C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

alignment_scores:
Quality: 61.00 Length: 18
Ratio: 4.067 Gaps: 0
Percent Similarity: 83.333 Percent Identity: 61.111

alignment_block:
US-09-198-779B-1 x F86862 ..

Align seg 1/1 to: F86862 from: 1 to: 399

```
169 AAGACCGCGCATACGCGCACTTGGCCGTGACGACGCCGACTTCACCTG 218
      ::::::::::::::::::::::::::::::::::::
368 GlnThrAlaAlaPheGlyHisPheGlyArgThrAspValGluLeuProTr 384

219 CGAG 222
      |||
384 pGlu 385
```

seq_name: p1r2:AD1654

seq_documentation_block:

S-methionine adenosyltransferase homolog metk [imported] - *Listeria innocua* (strain Clif
C:Species: *Listeria innocua*
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AD1654
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Ertlan, K.D.; Fsihl, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehl
A:Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1654
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1399 <G1A>
A:Cross-references: GB:ML520222; PIDN:CAC97004.1; PID:g164114260; GSPDB:GN00178
A:Experimental source: strain Clif11262
C:Genetics:
A:Gene: metk
C:Superfamily: methionine adenosyltransferase

alignment_scores:
Quality: 61.00 Length: 18
Ratio: 4.067 Gaps: 0
Percent Similarity: 83.333 Percent Identity: 61.111

alignment_block:

US-09-198-779B-1 x AD1654 ..

Align seg 1/1 to: AD1654 from: 1 to: 399

```
169 AAGACCGCGCATACGCGCACTTGGCCGTGACGACGCCGACTTCACCTG 218
      ::::::::::::::::::::::::::::::::::::
368 GlnThrAlaAlaPheGlyHisPheGlyArgThrAspValGluLeuProTr 384

219 CGAG 222
      |||
384 pGlu 385
```

seq_name: p1r2:AH1282

seq_documentation_block:

S-methionine adenosyltransferase homolog metk [imported] - *Listeria monocytogenes* (stra
C:Species: *Listeria monocytogenes*
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AH1282

R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloek
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Ertlan, K.D.; Fsihl,
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkai, G.; Madueno, E.; Maitournam, A.;
ok, C.; Schluter, T.; Simes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehl
A:Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1282
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1399 <G1A>
A:Cross-references: GB:NC_003210; PIDN:CAC99742.1; PID:g16411100; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: metk
C:Superfamily: methionine adenosyltransferase

alignment_scores:
Quality: 61.00 Length: 18
Ratio: 4.067 Gaps: 0
Percent Similarity: 83.333 Percent Identity: 61.111

alignment_block:

US-09-198-779B-1 x AH1282 ..

Align seg 1/1 to: AH1282 from: 1 to: 399

```
169 AAGACCGCGCATACGCGCACTTGGCCGTGACGACGCCGACTTCACCTG 218
      ::::::::::::::::::::::::::::::::::::
368 GlnThrAlaAlaPheGlyHisPheGlyArgThrAspValGluLeuProTr 384

219 CGAG 222
      |||
384 pGlu 385
```

seq_name: p1r2:F70899

seq_documentation_block:

Probable metk protein - *Mycobacterium tuberculosis* (strain H37RV)
C:Species: *Mycobacterium tuberculosis*
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C:Accession: F70899
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garrier, T.; Churcher, C.; Harris, D.; Gordon
.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete gen
A:Reference number: A70500; MUID:98295987
A:Accession: F70899
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-403 <COL>
A:Cross-references: GB:Z80108; GB:AL123456; NID:g3256012; PIDN:CAB02194.1; PID:g32561
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: metk
C:Superfamily: methionine adenosyltransferase

alignment_scores:
Quality: 61.00 Length: 20
Ratio: 4.067 Gaps: 0
Percent Similarity: 75.000 Percent Identity: 55.000

alignment_block:

US-09-198-779B-1 x F70899 ..

Align seg 1/1 to: F70899 from: 1 to: 403

```
163 TTCATCAGACCGCGCATACGCGCACTTGGCCGTGACGACGCCGACTT 212
```

```

::: ||||||||||||||||||||| |||:::
372 TyraLProthraLaLaTyGlyHIsPheGlyTrGThrsPaLaGluLe 388
213 CAACTGGAG 222
388 uProTPrGlu 391
seq_name: p1r2:B97403

```

seq_documentation_block:

```

methionine adenosyltransferase (EC 2.5.1.6) - Agrobacterium tumefaciens (strain C58, Gen
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
C:Accession: B97403
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; PMID:11743194
A:Accession: B97403
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-420 <KUR>
A:Cross-references: GB:AE007869; PIDN:AAK86179.1; PID:g15155274; GSPDB:GN00169
C:Genetics:
A:Gene: AGR_C_632
A:Note: Agrobacterium circular chromosome
A:Map position: methionine adenosyltransferase
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

```

alignment_scores:

Quality:	61.00	Length:	30
Ratio:	2.905	Gaps:	2
Percent Similarity:	70.000	Percent Identity:	46.667

alignment_block:

```

US-09-198-779b-1 x B97403 ..
Align seg 1/1 to: B97403 from: 1 to: 420

```

```

163 TTCATCAAGACCGCCGATACGCCACTTGGCCGTGAC.....GA 203
::: |||||||:::|||||||||
384 TyraLaLysThrSerTyrGlyHIsPheGlyTrGThrsPaLaGlyArgAs 400
204 GCCGCACTTCACCTGGCAG.....GTGGCAAGCCC 234
|:::|||||::: |||
400 pGlySerPheSerTPrGluLysLeuAspLeuValLysPro 413

```

seq_name: p1r2:AB2621

seq_documentation_block:

```

S-adenosylmethionine synthetase metK [imported] - Agrobacterium tumefaciens (strain C58,
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C:Accession: AB2621
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Moo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, B.W.
A:Title: The genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AB2621
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-420 <KUR>
A:Cross-references: GB:AE008688; PIDN:ALA1384.1; PID:g17738701; GSPDB:GN00186
C:Experimental source: strain C58 (Dupont)
A:Genetics:
A:Gene: metK
A:Map position: circular chromosome

```

C:Superfamily: methionine adenosyltransferase

alignment_scores:	Quality:	61.00	Length:	30
Ratio:	2.905	Gaps:	2	
Percent Similarity:	70.000	Percent Identity:	46.667	

alignment_block:

```

US-09-198-779b-1 x AB2621 ..
Align seg 1/1 to: AB2621 from: 1 to: 420

```

```

163 TTCATCAAGACCGCCGATACGCCACTTGGCCGTGAC.....GA 203
::: |||||||:::|||||||||
384 TyraLaLysThrSerTyrGlyHIsPheGlyTrGThrsPaLaGlyArgAs 400
204 GCCGCACTTCACCTGGCAG.....GTGGCAAGCCC 234
|:::|||||::: |||
400 pGlySerPheSerTPrGluLysLeuAspLeuValLysPro 413

```

seq_name: p1r2:AC2211

seq_documentation_block:

```

heme transport protein alr3242 [imported] - Anabaena sp. (strain PCC 7120)
C:Species: Anabaena sp.
A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
C:Accession: AC2211
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu
Nakazaki, N.; Shimpou, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AC2211
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-877 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA874941.1; PID:g17132337; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr3242

```

alignment_scores:	Quality:	61.00	Length:	36
Ratio:	2.346	Gaps:	0	
Percent Similarity:	72.222	Percent Identity:	36.111	

alignment_block:

```

US-09-198-779b-1 x AC2211 ..
Align seg 1/1 to: AC2211 from: 1 to: 877

```

```

12 AACCTCGGTGGACAGATCGACGCTGCCATGCTGAATGAAGCAGGTCT 61
||||||| ||| ||| :::
412 SerLeuGlyTyrGlnTyrAspAsnProAsnSerLysSerTPrLeuGlnPh 428
62 GATCCATTGTCGTGTTATTAAATGTTAAATTAATGACGACACACA 111
:::|||||::: ||| :::|||||:::|||||
428 eValAlrGaLaAsnLeuTyrTyrGlnAsnAlaLeuIleGluGluAspSerA 445
112 CACGTACG 119
:::||||:
445 snArgSer 447

```

seq_name: p1r2:S74736

seq_documentation_block:

```

methionine adenosyltransferase (EC 2.5.1.6) - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803

```

C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C/Accession: S74736
R/Keneo, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A/Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
s.
A/Reference number: S74322; MUID:97061201
A/Accession: S74736
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-409 <KAN>
A/Cross-references: EMBL:D90901; GB:AB001339; NID:g1651897; PIDN:BAAL6887.1; PID:g165196
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C/Genetics:
A/Gene: metX
A/Start codon: GTG
C/Superfamily: methionine adenosyltransferase
C/Keywords: S-adenosylmethionine; transferase

alignment_scores:
Quality: 60.50 Length: 22
Ratio: 3.559 Gaps: 1
Percent Similarity: 77.273 Percent Identity: 59.091

alignment_block:
US-09-198-779B-1 x S74736 ..

Align seg 1/1 to: S74736 from: 1 to: 409

160 AGGTCATCAAG...ACCGCGCATACGCGCCTTGCGCGAGACGAC 206
||||| : : : ||||||| ||||||| : : : |||
367 ArgPheTYrGLNAspValAlaIleTYrGLNAspValAlaIle 383
207 CGACTTCACCTGCGAG 222
||||| : : : |||
383 uAspLeuProTYrGlu 388

seq_name: pir2:E82319

seq_documentation_block:
S-adenosylmethionine synthase VC0472 [imported] - *Vibrio cholerae* (strain N16961 serogroup C)
C/Species: *Vibrio cholerae*
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C/Accession: E82319
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
Chardson, D.; Ermolaeva, M.D.; Yamathavan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A/Reference number: AB2035; MUID:20406833
A/Accession: E82319
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-385 <HEI>
A/Cross-references: GB:AE004133; GB:AE003852; NID:99654889; PIDN:AAF93645.1; GSPDB:GN001
C/Experimental source: serogroup O1, strain N16961, biotype El Tor
C/Genetics:
A/Gene: VC0472
A/Map position: 1
C/Superfamily: methionine adenosyltransferase

alignment_scores:
Quality: 60.00 Length: 12
Ratio: 5.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 83.333

alignment_block:
US-09-198-779B-1 x E82319 ..

Align seg 1/1 to: E82319 from: 1 to: 385

169 AAGACCGCGATACGCGCCTTGCGCGAGAC 204
||||| : : : ||||||| ||||||| : : : |||
355 LysThrAlaIleTYrGLNAspValAlaIleTYrGLNAspValAlaIle 366

seq_name: pir2:B84381

seq_documentation_block:
acylaminoacyl-peptidase [imported] - *Halobacterium* sp. NRC-1
C/Species: *Halobacterium* sp. NRC-1
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C/Accession: B84381
R/Nb, W.V.; Kennedy, S.P.; Mahatras, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,
J.; Leitauer, B.; Keller, K.; Cruz, R.; Dawson, M.J.; Hough, D.W.; Maddocks, D.G.; J.
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A/Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.;
A/Title: Genome sequence of *Halobacterium* species NRC-1.
A/Reference number: AB4160; MUID:20504483
A/Accession: B84381
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-674 <STO>
A/Cross-references: GB:AE004437; NID:g10581715; PIDN:AAG20414.1; GSPDB:GN00138
C/Genetics:
A/Gene: yuxL

alignment_scores:
Quality: 60.00 Length: 87
Ratio: 1.579 Gaps: 3
Percent Similarity: 43.678 Percent Identity: 28.736

alignment_block:
US-09-198-779B-1/rev x B84381 ..

Align seg 1/1 to: B84381 from: 1 to: 674

228 GACCACTCGCGAGTGCAGTGGCGCGCGCAAGCGCGTATG 179
||||| : : : ||||||| ||||||| : : : |||
183 AspLeuAlaIleGLYArgValAlaAspArgValThrAlaIleGLYAlaIle 199
178 CGCG.....GACCTGNNNNNNNNNNNNNNNNNN 175
199 SGLYLYProAlaTYrGLYAspAspGLYThrLeuTYrTYrProIleArg 216
174 ..GGCTTGAT.....GACCTGNNNNNNNNNNNNNNNNNN 142
||||| : : : ||| : : : ||| : : : |||
216 rGLYLeuAspAlaAspAspArgLeuGLYTrpAlaIleGLYAlaIleThr 232
141 NNNNNNNNNNNNNNNNNNNNAACGTACTGTGTCTCTGCTCAATTATA 92
::: : : : : : |||
233 ProAlaAspSerAlaAspSerThrValVal..... 242
91 CAACATTAATAACACACAAATGATCAGACCTGCATTATTCAGC 42
||||| : : : ||| : : : ||| : : : |||
243ThrThrValGLYGLYMetClyProThrLeuAlaValH 255
41 ATGGCGACGCT 31
||||| : : : |||
255 ISGLYSerArg 258

seq_name: pir2:A71281

seq_documentation_block:
probable S-adenosylmethionine synthetase (metX) - *Syphilis spirochete*
C/Species: *Treponema pallidum* subsp. *pallidum* (*Syphilis spirochete*)
C/Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 18-Jun-1999
C/Accession: A71281
R/Praser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.;
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.;
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998

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OM of: US-09-198-779b-1 to: SPTREMBL_19.* out_format : pfs
Date: Aug 20, 2002 2:59 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:

```
-MODEL=framed+ncp_model -DEV=xlp  
-O=/cgcn2.1/USPRO_pool/US09198779/runatc_19082002_140913_25160/app-query.fasta.1.296  
-DB=SPTREMBL_19 -QFMT=fastan -SUFFIX=rspt -GAPOP=12.000  
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPL=0.000 -LOOPEXT=0.000  
-GAPOP=4.500 -GAPEXT=0.050 -YGAPEXT=10.000 -YGAPEXT=0.500  
-YGAPEXT=6.000 -YGAPEXT=7.000 -YGAPEXT=10.000 -YGAPEXT=0.500  
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blissum62  
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pc  
-THR_MAX=100 -THR_MIN=0 -ALIGN=45 -MODE=LOCAL -OUTFMT=pls  
-NORMEXT -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09198779 -CGCN1.1.113 -NCPU=6 -ICPU=3 -LONGLOG  
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPHY -WAIT -THREADS=1
```

Search information block:

Query: US-09-198-779b-1
Query length: 235
Database: SPTREMBL_19.*
Database sequences: 562222
Database length: 172994929
Search time (sec): 51.790000

score_list:

Sequence	Strd	Orig	ZScore	EScore	Len	Document
sp_plant:Q41961	+	125.00	338.61	1.1e-09	54	Q41961 arabidopsis thaliana (mou
sp_plant:Q9FVU1	+	125.00	310.87	1.5e-09	393	Q9FVU1 brassica juncea (leaf mu
sp_plant:Q9LUT2	+	125.00	310.87	1.5e-09	393	Q9LUT2 arabidopsis thaliana (mou
sp_plant:Q42242	+	122.00	320.25	3.1e-09	56	Q42242 arabidopsis thaliana (mou
sp_plant:Q944U4	+	122.00	302.79	4.1e-09	395	Q944U4 dendrobium crumenatum (t
sp_plant:Q94C00	+	121.00	314.38	4.6e-09	80	Q94C00 elaeis oleifera s-adenos
sp_plant:Q9S807	+	121.00	300.15	5.8e-09	393	Q9S807 petunia hybrida (petunia
sp_plant:Q9S992	+	120.00	313.16	6.3e-09	68	Q9S992 brassica napus (rape). me
sp_plant:Q941A8	+	120.00	298.06	8.0e-09	368	Q941A8 arabidopsis thaliana (mou
sp_plant:Q9FEE0	+	120.00	297.47	8.1e-09	393	Q9FEE0 arabidopsis thaliana (mou
sp_plant:Q94FR6	+	120.00	297.47	8.1e-09	393	Q94FR6 brassica juncea (leaf mu
sp_plant:Q94FR4	+	120.00	297.47	8.1e-09	393	Q94FR4 brassica juncea (leaf mu
sp_plant:Q9AT55	+	116.00	294.80	1.1e-08	393	Q9AT55 elaeagnus umbellata. s-s
sp_plant:Q9SANA9	+	116.00	297.75	2.7e-08	115	Q9SANA9 catharanthus roseus (ros
sp_plant:Q9SUI8	+	115.00	284.15	4.5e-08	390	Q9SUI8 arabidopsis thaliana (mou
sp_plant:Q9AT56	+	115.00	284.08	4.5e-08	393	Q9AT56 elaeagnus umbellata. s-s
sp_plant:Q94FR5	+	114.00	281.47	6.4e-08	390	Q94FR5 brassica juncea (leaf mu
sp_plant:Q9LUG6	+	113.00	278.66	9.0e-08	396	Q9LUG6 oryza sativa (rice). s-s
sp_plant:Q9FVU7	+	111.00	273.57	1.8e-07	393	Q9FVU7 pinus contorta (shore pi
sp_plant:Q9FVU6	+	111.00	273.52	1.8e-07	393	Q9FVU6 suada maritima subsp. s
sp_plant:Q92J30	+	101.00	253.61	4.9e-06	179	Q92J30 chlamydomonas reinhardtii
sp_plant:Q9S805	+	101.00	246.65	5.5e-06	390	Q9S805 petunia hybrida (petunia
sp_plant:Q9LUD7	+	100.00	243.91	7.8e-06	393	Q9LUD7 camelina sinensis (tea).
sp_plant:Q9M7R8	+	97.00	235.94	2.2e-05	390	Q9M7R8 nicotiana tabacum (commo
sp_invertebrate:Q9GN14	+	75.00	176.74	0.0421	402	Q9GN14 plasmodium falciparum
sp_bacteriophage:Q9JY09	+	72.00	169.00	0.1175	389	Q9JY09 neisseria meningitidis
sp_bacteriophage:Q9JYV6	+	72.00	169.00	0.1175	389	Q9JYV6 neisseria meningitidis
sp_bacteriophage:Q9LUV3	+	71.00	166.03	0.1664	402	Q9LUV3 streptococcus coelicolor
sp_bacteriophage:Q938W7	+	71.00	155.92	0.1667	407	Q938W7 streptococcus fradiae. me
sp_bacteriophage:Q9K5M4	+	67.00	152.89	0.6588	407	Q9K5M4 corynebacterium glutamic
sp_bacteriophage:Q988A0	+	66.00	152.89	0.9234	391	Q988A0 rhizobium loti (mesorhiz
sp_bacteriophage:Q9AC18	+	64.50	148.51	1.35	407	Q9AC18 caulobacter crescentus.
sp_bacteriophage:Q9P077	+	64.00	146.76	1.86	376	Q9P077 ureaplasma parvum (urea
sp_bacteriophage:Q92S14	+	64.00	131.69	2.59	1979	Q92S14 rhizobium meliloti (sind
sp_rodent:Q98196	-	63.50	141.76	2.75	395	Q98196 mus musculus (mouse). m
sp_rodent:Q99459	+	63.00	141.76	2.75	395	Q99459 mus musculus (mouse). pu
sp_bacteriophage:Q9A718	+	63.00	141.19	2.75	589	Q9A718 caulobacter crescentus.
sp_bacteriophage:Q98P00	+	61.00	139.84	5.11	376	Q98P00 mycoplasma pulmonis. s-s
sp_plant:Q9FVU8	+	61.00	139.56	5.14	388	Q9FVU8 pinus contorta (shore pi
sp_bacteriophage:Q99T79	+	61.00	139.33	5.16	398	Q99T79 staphylococcus aureus (s

sp_bacteriophage:Q9K709	+	61.00	139.31	5.16	399	Q9K709 bacillus halodurans.
sp_bacteriophage:Q92A25	+	61.00	139.31	5.16	399	Q92A25 listeria innocua. me
sp_bacteriophage:Q9KUP3	+	60.00	136.95	7.24	385	Q9KUP3 vibrio cholerae. s-s
sp_archaeal:Q9H07	-	60.00	131.95	7.86	674	Q9H07 halobacterium sp. (s
sp_invertebrate:Q9VE57	-	60.00	119.53	9.63	2703	Q9VE57 drosophila melano

seq_name: sp_plant:Q41961

seq_documentation_block:

```
ID Q41961 PRELIMINARY; PRT; 54 AA.  
AC Q41961;  
DT 01-NOV-1996 (TREMBLER, 01, Created)  
DT 01-NOV-1996 (TREMBLER, 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLER, 19, Last annotation update)  
DE S-ADENOSYLMETHIONINE SYNTHETASE 2 (FRAGMENT).  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eucotsids II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV, COLUMBIA; TISSUE=SEEDLING;  
RA Desprez T., Amselem J., Chapelle H., Rouze P., Caboche M., Hofte H.;  
RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.  
DR EMBL: Z18777; CA79253.1; -.  
DR InterPro: IPR002133; S-Adomet_synth.  
DR Pfam: PF00438; S-Adomet_synth.1;  
DR TrEMBL: P02773; S-Adomet_synth.1;  
FT NON_TER 1  
SQ SEQUENCE 54 AA; 5999 MW; 73FB9A625D54DD78 CRC64;
```

alignment_scores:

Quality: 125.00 Length: 25
Ratio: 5.208 Gaps: 0
Percent Similarity: 96.000 Percent Identity: 92.000

alignment_block:

US-09-198-779b-1 x Q41961 ..

Align seg 1/1 to: Q41961 from: 1 to: 54

```
160 AGTCATCATAGACCGCCGATACGCGCATTGGCGGTAGACGCCGA 209  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
22 ArgpneleulysThralalatalyrglyhlsphneglyArgAspaspAlans 38  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
210 CTTGACCTCGAGGTCGACGCC 234  
38 pPherhTrpGluValValyspro 46
```

seq_name: sp_plant:Q9FVU1

seq_documentation_block:

```
ID Q9FVU1 PRELIMINARY; PRT; 393 AA.  
AC Q9FVU1;  
DT 01-MAR-2001 (TREMBLER, 16, Created)  
DT 01-MAR-2001 (TREMBLER, 16, Last sequence update)  
DT 01-DEC-2001 (TREMBLER, 19, Last annotation update)  
DE S-ADENOSYLMETHIONINE SYNTHETASE.  
OS Brassica juncea (leaf mustard) (Indian mustard).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eucotsids II; Brassicales; Brassicaceae; Brassica.  
OX NCBI_TaxID=3707;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Liu J.-Z., Pua E.-C.;  
RT "Sequencing of a s-adenosylmethionine Synthetase Genomic Clone from  
Brassica Juncea."  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF271220; AAG17666.1; -.  
DR HSSP; P04384; IMXB.
```


|||||||
40 pperhrrtprgluValValysPro 48

seq_name: sp_plant:Q944U4

seq_documentation_block:
ID Q944U4 PRELIMINARY; PRT; 395 AA.

AC Q944U4;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
DE S-ADENOSYL-L-METHIONINE SYNTHETASE.

GN SAMS.

OS Dendrobium crumenatum (Tropical pigeon orchid).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Orchidaceae;

OC Epidendroideae; higher Epidendroideae; Dendrobieae; Dendrobinae;

OC Dendrobium.

OC NCBI_TaxID=51096;

OX [1]

RP SEQUENCE FROM N.A.

RA Han P., Pua E.C.;

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF20238; AAL16064.1; .

SQ SEQUENCE 395 AA; 43210 MW; 240AA4A7CF8DA440 CRC64;

alignment_scores:

Quality: 122.00 Length: 25

Ratio: 5.304 Gaps: 0

Percent Similarity: 92.000 Percent Identity: 92.000

alignment_block:

US-09-198-779b-1 x Q944U4 ..

Align seg 1/1 to: Q944U4 from: 1 to: 395

160 AGGTCATCATAGAGCCGCGCATACGCGCATTGGCCGTGACGAGCCGA 209

|||||

363 ArgpHeuLeuYstHrAlaIatYrgLHsPheGlyArgAspAspPhras 379

210 CTTACCTGCGAGGTGTCACGCC 234

|||||

379 pperhrrtprgluValValysPro 387

seq_name: sp_plant:Q94C00

seq_documentation_block:

ID Q94C00 PRELIMINARY; PRT; 80 AA.

AC Q94C00;

DT 01-DEC-2001 (TRENBLREL. 19, Created)

DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)

DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)

DE S-ADENOSYL METHIONINE SYNTHETASE (FRAGMENT).

GN SAMS1.

OS Elaeis oleifera.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Arecaceae; Arecoidae;

OC Coccolae; Elaeidinae; Elaeis.

OC NCBI_TaxID=80265;

OX [1]

RP SEQUENCE FROM N.A.

RA Bhoire S.J., Shah F.H.;

RT "Isolation of S-adenosyl-L-methionine synthetase (SAMS1) cDNA clone

from oil palm (Elaeis oleifera) mesocarp tissue."

RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY039010; AAK72126.1; .

FT NON_TER 1 1

SQ SEQUENCE 80 AA; 8983 MW; B1F012583F825776 CRC64;

alignment_scores:

Quality: 121.00 Length: 25

Ratio: 5.042 Gaps: 0
Percent Similarity: 96.000 Percent Identity: 88.000

alignment_block:

US-09-198-779b-1 x Q94C00 ..

Align seg 1/1 to: Q94C00 from: 1 to: 80

160 AGGTCATCATAGAGCCGCGCATACGCGCATTGGCCGTGACGAGCCGA 209

|||||

48 ArgpHeuLeuYstHrAlaIatYrgLHsPheGlyArgAspAspPhras 64

210 CTTACCTGCGAGGTGTCACGCC 234

|||||

64 pperhrrtprgluValValysPro 72

seq_name: sp_plant:Q9SBQ7

seq_documentation_block:

ID Q9SBQ7 PRELIMINARY; PRT; 393 AA.

AC Q9SBQ7;

DT 01-MAY-2000 (TRENBLREL. 13, Created)

DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)

DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)

DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE

ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).

OS Petunia hybrida (Petunia).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.

OC NCBI_TaxID=4102;

OX [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CV. VIOLET; TISSUE=COROLLA;

RX MEDLINE=20027448; PubMed=10557255;

RA Soong S.C., To K.Y.;

RT "Nucleotide sequence of A cDNA (AF170798) Encoding Type I S-

Adenosyl-L-methionine Synthetase from Petunia hybrida. (PGR99-160).";

RL Plant Physiol. 121:1053-1053(1999).

-1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM

METHIONINE AND ATP (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +

PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.

CC -1- PATHWAY: ACTIVATED METHYL CYCLE.

CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.

DR EMBL; AF170798; AAD48485.1; .

DR HSSP; P04384; 1MB.

DR InterPro; IPR002133; S-Adomet_synth.

DR Pfam; PF00438; S-Adomet_synth. 1.

DR Pfam; PF02772; S-Adomet_synth2; 1.

DR Pfam; PF02773; S-Adomet_synth3; 1.

DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.

DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.

DR ATP-binding; One-carbon metabolism; Transferrase.

FW ATP-binding; One-carbon metabolism; Transferrase.

SQ SEQUENCE 393 AA; 43169 MW; 0AC0DD62F28F6749 CRC64;

alignment_scores:

Quality: 121.00 Length: 25

Ratio: 5.042 Gaps: 0

Percent Similarity: 96.000 Percent Identity: 88.000

alignment_block:

US-09-198-779b-1 x Q9SBQ7 ..

Align seg 1/1 to: Q9SBQ7 from: 1 to: 393

160 AGGTCATCATAGAGCCGCGCATACGCGCATTGGCCGTGACGAGCCGA 209

|||||

361 ArgpHeuLeuYstHrAlaIatYrgLHsPheGlyArgAspAspPhras 377

210 CTTACCTGCGAGGTGTCACGCC 234

|||||

Shinozaki K., Davis R.W., Theologis A., Ecker J.P.:

DR InterPro; IPR002133;

DR InterPro: IPR002133; S-Adomet_synt.
DR Pfam: PF00438; S-Adomet_synt; 1.
DR Pfam: PF02772; S-Adomet_syntd2; 1.

```

DR Pfam: PF02773; S-Adomet_synth3: 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
SQ SEQUENCE 393 AA; 43158 MW; 27B0AF8AF55D2FF3 CRC64;

alignment_scores:
Quality: 120.00 Length: 25
Ratio: 5.217 Gaps: 0
Percent Similarity: 92.000 Percent Identity: 88.000

Alignment_block:
US-09-198-779B-1 x Q9FEEO ..

Align seg 1/1 to: Q9FEEO from: 1 to: 393

160 AGCTTCATCAAGACCGCCGATACGCGCCATTGGCCGTGACGACGCCGA 209
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
361 ArgpHeLeuLysThrAlaIatYrGlyHISpHeGlyArgAspAspProAs 377
210 CTTACCTGCGAGGTGTCACGCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
377 pHeHrTrpGluValValLysPro 385

seq_name: sp_plant:Q94FA6

seq_documentation_block:
ID Q94FA6 PRELIMINARY; PRT; 393 AA.
AC Q94FA6:
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE S-ADENOSYLMETHIONINE SYNTHETASE.
GN MSAMS.
OS Brassica juncea (Leaf mustard) (Indian mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID=3707;
RN [1]
RP SEQUENCE FROM N.A.
RT Pua E.C., Lim C.C., Liu J.Z.;
RT "Molecular cloning of S-adenosylmethionine genes from mustard.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF379013; AAK71233.1; -.
SQ SEQUENCE 393 AA; 43141 MW; E7598AC6BD44A0EB CRC64;

alignment_scores:
Quality: 120.00 Length: 25
Ratio: 5.217 Gaps: 0
Percent Similarity: 92.000 Percent Identity: 88.000

Alignment_block:
US-09-198-779B-1 x Q94FA6 ..

Align seg 1/1 to: Q94FA6 from: 1 to: 393

160 AGTTCATCAAGACCGCCGATACGCGCCATTGGCCGTGACGACGCCGA 209
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
361 ArgpHeLeuLysThrAlaIatYrGlyHISpHeGlyArgAspAspProAs 377
210 CTTACCTGCGAGGTGTCACGCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
377 pHeHrTrpGluValValLysPro 385

seq_name: sp_plant:Q94FA6

seq_documentation_block:
ID Q94FA6 PRELIMINARY; PRT; 393 AA.
AC Q94FA6:
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE
ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).
GN SAMS2.
OS Elaeagnus umbellata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae
OC eurosids I; Rosales; Elaeagnaceae; Elaeagnus.
NCBI_TaxID=43233;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=ROOT NODULE;
RA Lee S., An C.;
RT "Structures and expression patterns of two cDNA clones encoding S-
adenosyl-L-methionine synthetase from the root nodule of Elaeagnus
umbellata.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
METHIONINE AND ATP (BY SIMILARITY).
CC CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE
CC PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
DR EMBL; AF346306; AAK29410.1; -.
DR HSSP; P04384; IMXB.
DR InterPro; IPR002133; S-Adomet_synth.
DR Pfam; PF00438; S-Adomet_synth; 1.
DR Pfam; PF02772; S-Adomet_synth2; 1.
DR Pfam; PF02773; S-Adomet_synth3; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
DR ATP-binding; One-carbon metabolism; Transferrase.

```

seq_name: sp_plant:Q9SJL8

ATP-binding; One-carbon metabolism; Transferase, 300 AA: 43A07.WT. EC09D48838E0C104 00CC4 SEQUENCE

160 AGTTATCATAGACCCGCCATACGGCCACTTTCGCGGTAGACAGCCCCA **209**

| | | | | | | | | | | | | | | | | | | | | |

361 ArgPheGlnIysThrAlaIatylrgLHisPheGIyrtgAsparProAs **377**

Ratio: 4.913 Gaps: 0
Percent Similarity: 92.000 Percent Identity: 80.000
alignment_block:
US-09-198-779b-1 x Q9L6U6 ..
Align seg 1/1 to: Q9L6U6 from: 1 to: 396
160 AGGTTATCAAGACCGCCGATACGGCCACTTTGGCCGTGACGACGCCGA 209
||||| |
364 ArgyleuylsthrAlaAlaIatYrGlyHisPheGlyArgAspAspProAs 380
210 CTTCACCTCGAGGTGTGTCAGACCC 234
||||| |
380 pphenThrTrpGluValValysPro 388
seq_name: sp_plant:Q9FVG7
seq_documentation_block:
ID Q9FVG7 PRELIMINARY; PRT; 393 AA.
AC Q9FVG7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6).
GN SAMS2.
OS Pinus concolor (Shore pine) (Lodgepole pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3339;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21380671; PubMed=11488480;
RA Lindroth A.M., Saarikoski P., Flyv G., Clapham D., Gronroos R.,
RA Thelander M., Rönne H., von Arnold S.;
RT "Two S-adenosylmethionine synthetase-encoding genes differentially
RT expressed during adventitious root development in Pinus concolora.";
RL Plant Mol. Biol. 46:335-346 (2001).
DR EMBL: AF187821; AAG17036.1;
DR HSSP: P04384; IMXB.
DR InterPro: IPR002133; S-Adomet_synt.
DR Pfam: PF00438; S-Adomet_synt; 1.
DR Pfam: PF02772; S-Adomet_syntd2; 1.
DR Pfam: PF02773; S-Adomet_syntd3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
KW Transferase
SO SEQUENCE 393 AA; 43068 MW; 5824C18313820F30 CRC64;
alignment_scores:
Quality: 111.00 Length: 25
Ratio: 5.045 Gaps: 0
Percent Similarity: 88.000 Percent Identity: 84.000
alignment_block:
US-09-198-779b-1 x Q9FVG7 ..
Align seg 1/1 to: Q9FVG7 from: 1 to: 393
160 AGGTTATCAAGACCGCCGATACGGCCACTTTGGCCGTGACGACGCCGA 209
||||| |
361 ArgPheGlnIysThrAlaAlaIatYrGlyHisPheGlyArgAspAspProAs 377
210 CTTCACCTCGAGGTGTGTCAGACCC 234
||||| |
377 pphenThrTrpGluThrValysPro 385
seq_name: sp_plant:Q9FPL6
seq_documentation_block:
ID Q9FPL6 PRELIMINARY; PRT; 395 AA.
AC Q9FPL6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE S-ADENOSYLMETHIONINE SYNTHETASE 2.
OS Suaeda maritima subsp. salsa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Suaeda.
OX NCBI_TaxID=126914;
RN [1]
RP SEQUENCE FROM N.A.
RA Ma X., Zhang H.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF321001; AAG42490.1; .
DR HSSP: P04384; IMXB.
DR InterPro: IPR002133; S-Adomet_synt.
DR Pfam: PF00438; S-Adomet_synt; 1.
DR Pfam: PF02772; S-Adomet_syntd2; 1.
DR Pfam: PF02773; S-Adomet_syntd3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
KW NON_TER
SO SEQUENCE 395 AA; 43008 MW; 8901451D723988D8 CRC64;
alignment_scores:
Quality: 111.00 Length: 25
Ratio: 5.045 Gaps: 0
Percent Similarity: 88.000 Percent Identity: 84.000
alignment_block:
US-09-198-779b-1 x Q9FPL6 ..
Align seg 1/1 to: Q9FPL6 from: 1 to: 395
160 AGGTTATCAAGACCGCCGATACGGCCACTTTGGCCGTGACGACGCCGA 209
||||| |
361 ArgPheGlnIysThrAlaAlaIatYrGlyHisPheGlyArgAspAspProAs 377
210 CTTCACCTCGAGGTGTGTCAGACCC 234
||||| |
377 pphenThrTrpGluThrValysPro 385
seq_name: sp_plant:O22350
seq_documentation_block:
ID O22350 PRELIMINARY; PRT; 179 AA.
AC O22350;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE S-ADENOSYLMETHIONINE SYNTHETASE (FRAGMENT).
GN CHRSAMS.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=137C;
RA Kim J.Y., Lee K.O., Lee S.H.;
RT "Chlamydomonas reinhardtii mRNA for S-adenosylmethionine synthetase.";
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF008568; AAB71853.1; .
DR HSSP: P04384; IMXB.
DR InterPro: IPR002133; S-Adomet_synt.
DR Pfam: PF00438; S-Adomet_synt; 1.
DR Pfam: PF02772; S-Adomet_syntd2; 1.
DR Pfam: PF02773; S-Adomet_syntd3; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
KW NON_TER
SO SEQUENCE 179 AA; 19459 MW; 76559D3E5C0E78B5 CRC64;
alignment_scores:
Quality: 101.00 Length: 24

Ratio: 4.810 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 79.167

alignment_block:

US-09-198-779B-1 x O22350 ..

Align seg 1/1 to: O22350 from: 1 to: 179

160 AGGTTTCATCAGACCGCGCATACGGCCATTGGCGGTGAGACGCCGA 209
|||||
153 ArglyrglnLysThrAlaIatyrGlyHisPheGlyArgAspAspProAs 169
210 CTTCACTGCGAGGTGTCAG 231
|||||
169 pPheThrTrpGluThrValLys 176

seq_name: sp-plant:Q9SBQ5

seq_documentation_block:

ID Q9SBQ5 PRELIMINARY; PRT; 390 AA.
AC Q9SBQ5;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE
ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).
GN SAM2.
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VIOLET; TISSUE=COROLLA;
RX PubMed=10759541;
RA Hsu Y.H., To K.Y.;
RT "Cloning of a cDNA (accession no. AF183891) encoding type II S-adenosyl-L-methionine synthetase from Petunia (PGR00-033).";
RL Plant Physiol. 122:1457-1457(2000).
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +
CC PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
DR EMBL: AF183891; AAD56396.1; -.
DR HSSP: P04384; IMXB.
DR InterPro: IPR002133; S-Adomet_synth.
DR Pfam: PF00438; S-Adomet_synth.1.
DR Pfam: PF02772; S-Adomet_synthd3; 1.
DR Pfam: PF02773; S-Adomet_synthd3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
KW ATP-binding; One-carbon metabolism; Transferrase.
SQ SEQUENCE 390 AA; 42593 MW; D46F4618732CA31 CRC64;

alignment_scores:

Quality: 101.00 Length: 24
Ratio: 4.810 Gaps: 0
Percent Similarity: 87.500 Percent Identity: 79.167

alignment_block:

US-09-198-779B-1 x Q9SBQ5 ..

Align seg 1/1 to: Q9SBQ5 from: 1 to: 390

160 AGGTTTCATCAGACCGCGCATACGGCCATTGGCGGTGAGACGCCGA 209
|||||
361 ArglyrglnLysThrAlaIatyrGlyHisPheGlyArgAspAspProAs 377
210 CTTCACTGCGAGGTGTCAG 231

|||||
377 pPheThrTrpGluThrValLys 384

seq_name: sp-plant:Q9LDQ7

seq_documentation_block:

ID Q9LDQ7 PRELIMINARY; PRT; 393 AA.
AC Q9LDQ7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE
ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).
GN SAM.
OS Camellia sinensis (Tea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Theaceae; Camellia.
OX NCBI_TaxID=4442;
RN [1]
RP SEQUENCE FROM N.A.
RA Feng Y.F., Liang Y.R.;
RT "Cloning of s-adenosylmethionine synthetase gene in tea plant.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAF;
RA Feng Y.F., Liang Y.R.;
RT "s-adenosylmethionine synthetase gene.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +
CC PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
DR EMBL: AJ277206; CAB83039.1; -.
DR EMBL: AB041534; BAA94605.1; -.
DR HSSP: P04384; IMXB.
DR InterPro: IPR002133; S-Adomet_synth.
DR Pfam: PF00438; S-Adomet_synth.1.
DR Pfam: PF02772; S-Adomet_synthd3; 1.
DR Pfam: PF02773; S-Adomet_synthd3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
KW ATP-binding; One-carbon metabolism; Transferrase.
SQ SEQUENCE 393 AA; 42800 MW; 67F3D2C50DA42682 CRC64;

alignment_scores:

Quality: 100.00 Length: 21
Ratio: 5.263 Gaps: 0
Percent Similarity: 90.476 Percent Identity: 85.714

alignment_block:

US-09-198-779B-1 x Q9LDQ7 ..

Align seg 1/1 to: Q9LDQ7 from: 1 to: 393

160 AGGTTTCATCAGACCGCGCATACGGCCATTGGCGGTGAGACGCCGA 209
|||||
361 ArgPheLeuLysThrAlaIatyrGlyHisPheGlyArgAspAspProAs 377

210 CTTCACTGCGAG 222
|||||
377 pPheThrTrpGlu 381

seq_name: sp-plant:Q9M7K8

seq_documentation_block:

ID Q9M7K8 PRELIMINARY; PRT; 390 AA.
AC Q9M7K8;
DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE
 ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 ON NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV, BURLEY 21; TISSUE=ROOT;
 RA Wang J., Tinko M.P.;
 RT "Cloning and Characterization of a cDNA Encoding S-Adenosyl-L-
 RT Methionine Synthetase, an enzyme involved in Polyamine Biosynthesis in
 RT Nicotiana tabacum L.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
 CC METHIONINE AND ATP (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +
 CC PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.
 CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
 CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
 DR EMBL: AF127243; RefSeq: AF42974.1; .
 DR HSSP: P04384; IMB.
 DR InterPro: IPR002133; S-Adomet_synth.
 DR Pfam: PF00438; S-Adomet_synth.1.
 DR Pfam: PF02772; S-Adomet_synthD2.1.
 DR Pfam: PF02773; S-Adomet_synthD3.1.
 DR PROSITE: PS00376; ADOMET_SYNTHETASE_1.1.
 DR PROSITE: PS00377; ADOMET_SYNTHETASE_2.1.
 DR ATP-binding; One-carbon metabolism; Transferrase.
 KW SEQUENCE 390 AA; 42715 MW; 2F7FD472B895D57A CRC64;
 SQ

alignment_scores: Quality: 97.00 Length: 24
 Ratio: 4.619 Gaps: 0
 Percent Similarity: 87.500 Percent Identity: 75.000

alignment block:
us-09-198-779b-1 x Q9M7K8 ..

Align seg 1/1 to: Q9M7K8 from: 1 to: 390

```

160 AGGTTTCATCAAGACCGCGCATGCGGCACTTGCGCGTGACGACGCCGA 209
||||: ||||||||| ||||||||| ||||||||| ||||||||| ||
361 ATGTyGlnlyThrAlaAlaIyTgLyHisPheGlyArgGaspProAs 377
210 CTTCACCTCGAGGTGTCAG 231
||||: |||||||||
377 pPheserTrpGluThrVallys 384
  
```

seq_name: sp_invertebrate:Q9GN14

seq_documentation_block:

ID Q9GN14 PRELIMINARY; PRT; 402 AA.
 AC Q9GN14;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DE S-ADENOSYLMETHIONINE SYNTHETASE (METHIONINE ADENOSYLTRANSFERASE)
 DE (EC 2.5.1.6).
 GN MAT.
 OS Plasmodium falciparum (isolate 3D7), and
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 ON NCBI_TaxID=36329, 5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.falciparum (isolate 3D7);
 RT MEDLINE=20036339; PubMed=10567242;
 RX

RA Chiang P.K., Chamberlin M.E., Nicholson D., Soudes S., Su X.,
 RA Subramanian G., Lanar D.E., Prigge S.T., Scovill J.P., Miller L.H.,
 RA Chou J.Y.;
 RT "Molecular characterization of Plasmodium falciparum S-
 RT adenosylmethionine synthetase.";
 RL Biochem. J. 344:571-576(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=P.falciparum; STRAIN=FCUP1/RSa;
 RA Clark K., Joubert F., Neitz A.W.H., Louw A.I.;
 RT "Molecular characterization of the Plasmodium falciparum methionine
 RT adenosyltransferase cDNA.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF097923; AF097923.1;
 DR EMBL: AF180426; AF02013.1; .
 DR HSSP: P04384; IMB.
 DR InterPro: IPR002133; S-Adomet_synth.
 DR Pfam: PF00438; S-Adomet_synth.1.
 DR Pfam: PF02772; S-Adomet_synthD2.1.
 DR Pfam: PF02773; S-Adomet_synthD3.1.
 DR PROSITE: PS00376; ADOMET_SYNTHETASE_1.1.
 DR TRANSFERASE.
 KW SEQUENCE 402 AA; 44844 MW; EB76C6023494A16C CRC64;
 SQ

alignment_scores: Quality: 75.00 Length: 23
 Ratio: 4.412 Gaps: 0
 Percent Similarity: 73.913 Percent Identity: 60.870

alignment block:
us-09-198-779b-1 x Q9GN14 ..

Align seg 1/1 to: Q9GN14 from: 1 to: 402

```

163 TTCATCAAGACCGCGCATGCGGCACTTGCGCGTGACGACGCCGACTT 212
||||: ||||||||| ||||||||| ||||||||| ||||||||| ||
369 pPheserTrpGluThrAlaAlaIyTgLyHisPheGlyArgGlnlySphRph 385
213 CACCTCGAGGTGTCAG 231
||||: |||||||||
385 ePhrTrpGluThrVallys 391
  
```

seq_name: sp_bacteriap:Q9JY09

seq_documentation_block:

ID Q9JY09 PRELIMINARY; PRT; 389 AA.
 AC Q9JY09;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-DEC-2001 (Tremblrel. 15, last sequence update)
 DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE
 DE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).
 GN METR OR NM01799.
 OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; Beta subdivision; Neisseriaceae; Neisseria.
 ON NCBI_TaxID=491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MC58 / SEROGROUP B;
 RX MEDLINE=20175755; PubMed=10710307;
 RA Tetzelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
 RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 RA Nelson W.C., Gwin M.L., Deboy R., Peterson J.D., Hickey E.K.,
 RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 RA Mason T., Ciecko A., Parksey D.S., Blair E., Ciltone H., Clark E.B.,
 RA Cotton M.D., Uitterlind T.R., Kouri H., Qin H., Vamathevan J.,
 RA Gill J., Scarlato V., Mastignani V., Pizzo M., Grandi G., Sun L.,
 RA Smith H.O., Fraser C.M., Moxon E.R., Rappunoli R., Venter J.C.;
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 RT MC58.";
 RL Science 287:1809-1815(2000).
 CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM

OC Phyllobacteriaceae; Mesorhizobium.
 RX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneke T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Kochizuki Y., Nakayama S., Nakazaki N., Shlimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 DR EMBL: AP003008; BAB52457.1;
 DR InterPro: IPR002133; S-Adomet_synt.
 DR Pfam: PF00438; S-Adomet_synt; 1.
 DR Pfam: PF02772; S-Adomet_synt2; 1.
 DR Pfam: PF02773; S-Adomet_synt3; 1.
 KM Complete proteome.
 SO SEQUENCE 391 AA; 42195 MW; 099E0643FE1B086D CRC64;

alignment_scores:
 Quality: 66.00 Length: 17
 Ratio: 4.400 Gaps: 0
 Percent Similarity: 88.235 Percent Identity: 64.706

alignment_block:
 us-09-198-779b-1 x Q98A80 ..

Align seg 1/1 to: Q98A80 from: 1 to: 391

```

172 ACCGCCGATACGCGCCTTGCGCGTGACGACGCCGACTTACCTGCGA 221
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
358 ThrAlaThrTyrGlyHisPheGlyArgGluGlnProGluPheThrIrp61 374
222 G 222
|
374 u 374

```

seq_name: sp_bacteriap:Q9AC18

seq_documentation_block:

ID Q9AC18 PRELIMINARY; PRT: 407 AA.

AC Q9AC18;

DT 01-JUN-2001 (Tremblrel. 17, Created)

DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE

DE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).

GN METK OR CC0050.

OS Caulobacter crescentus.

OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;

OC Caulobacter.

OX NCBI_TaxID=69394;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 19089 / CB15;

RX MEDLINE=21173698; PubMed=11259647;

RA Eelsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

RA DeBoy R.T., Dodson R.T., Durkin A.S., Gwin M.L., Haft D.H.,

RA Kotonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

RA Unterback T., Tran K., Wolf A., Vamathavan J., Ermolaeva M., White O.,

RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

RT "Complete genome sequence of Caulobacter crescentus.";

RT Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001)

CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM

CC METHIONINE AND ATP (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +

CC PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.

CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
 DR EMBL: AE005679; AKR22038.1;
 DR HSSP: P04384; IMXB.
 DR TIGR: CC0050;
 DR InterPro: IPR002133; S-Adomet_synt.
 DR Pfam: PF00438; S-Adomet_synt; 1.
 DR Pfam: PF02772; S-Adomet_synt2; 1.
 DR Pfam: PF02773; S-Adomet_synt3; 1.
 DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
 DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
 KM ATP-binding: Complete proteome; One-carbon metabolism: Transferase.
 SO SEQUENCE 407 AA; 43818 MW; E640BC115439FD92 CRC64;

alignment_scores:
 Quality: 64.50 Length: 72
 Ratio: 1.792 Gaps: 3
 Percent Similarity: 50.000 Percent Identity: 27.778

alignment_block:
 us-09-198-779b-1 x Q9AC18 ..

Align seg 1/1 to: Q9AC18 from: 1 to: 407

```

16 TCGGTGACAGATCGACGCTGCCATGCTGATTAATGACGCTCTGATC 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
344 AlaValLeuGluIysThrLeuProGlnLeuIleGlyGlyAlaThrProAr 360
66 CATGTGCTGTGTATTAATGTTGTAATTAATGACGACGACAGACAACAGC 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
360 galAlaIleArg.....GluHisL 366
116 TAGCTTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 165
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
366 euGlnLeuAsnArgProIle.....Tyr 373
166 ATCAGACCGCGCGCATACGCGCCTTGCGCGT.....GACGACGC 206
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
374 AlaArgThrAlaAlaIleTyrGlyHisPheGlyArgThrProAspAsnGluI 390
207 CGACTTCACCTCGCAG 222
: |||||: |||
390 yGlyPheSerTrpGlu 395

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seq_name: sp_bacteriap:Q9PQ77

seq_documentation_block:

ID Q9PQ77 PRELIMINARY; PRT: 376 AA.

AC Q9PQ77;

DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE

DE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).

GN METK OR U0412.

OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;

OC Mycoplasmataceae; Ureaplasma.

OX NCBI_TaxID=134821;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=SEROVAR 3;

RX MEDLINE=20500219; PubMed=11048724;

RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,

RA Cassell G.H.;

RT "The complete sequence of the mucosal pathogen ureaplasma

RT urealyticum.";

RT Nature 407:757-762(2000).

CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM

CC METHIONINE AND ATP (BY SIMILARITY).

Length: 30

1410	lyasinserseraspser.....	142
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alignment_scores:
 Quality: 63.00 Length: 61
 Ratio: 1.909 Gaps: 2
 Percent Similarity: 54.098 Percent Identity: 31.148
 alignment_block:
 US-09-198-79B-1 x Q9A718 ..
 Align seg 1/1 to: Q9A718 from: 1 to: 589
 53 GACGGTCCTGCATCATCTGTCGTTGCTATTATGTTGTTATATGAC 102
 |||||
 240 ASPLGYPROASP.....GL 245
 103 AGCACACAAACAGCTACGCTTNNNNNNNNNNNNNNNNNNNNNNNN 152
 |||
 245 nglYProMetThrHisGlnAlaArgAlaSnGlySerSerSerAlaG 262
 153 NNNNNNACAGTTCATCAAGACCGCGCAATACGCGCACTTGGCCGAG 202
 ::::|
 262 YAlaMetAlaSerSer..ProProIaGlnSerArgLeuAlaAlaasp 277
 203 AGCCGCACTTCACTCGCGAGGTGTCACAGCCCC 235
 ::|||
 278 AlaProAspAlaProAlaAlaThrSerSerPro 288
 seq_name: sp_bacteriap:Q98PMO
 seq_documentation_block:
 ID Q98PMO PRELIMINARY; PRN; 376 AA.
 AC Q98PMO;
 DT 01-OCT-2001 (TReMBLrel. 18, Created)
 DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
 DE S-ADEONOSYLMETHIONINE SYNTHETASE (METHIONINE ADEONOSYLTRANSFERASE)
 DE (ADONET SYNTHETASE) (EC 2.5.1.6).
 GN MYPU_7020.
 OS Mycoplasma pulmonis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 NC Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2107;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=UAB CTIP;
 RX MEDLINE=21267165; PubMed=11353084;
 RA Chambaud I., Hellig R., Ferris S., Barbe V., Samson D., Galisson F.,
 RA Moszer I., Dydvig K., Wroblewski H., Viari A., Rooha E.P.C.,
 RA Blanchard A.,
 RT "The complete genome sequence of the murine respiratory pathogen
 Mycoplasma pulmonis."

169 AAGACCGCGCATACGGCACTTTGGCCGTGACGACGCCGACTTCACCTG 218

2
 7
 1
 6
 5
 4
 3
 2
 1

383 pglu 384

seq_name: sp_bacteriap:Q9K7Q9

seq_documentation_block:
ID Q9K7Q9 PRELIMINARY; PRT; 399 AA.

AC Q9K7Q9;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE
GN METK OR BH3300.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE +
CC PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC EMBL; AP001518; BAB07019.1; -.
DR HSSP: P04384; 1FUG.
DR InterPro: IPR002133; S-Adomet_synth.
DR Pfam: PF00438; S-Adomet_synth.1.
DR Pfam: PF02772; S-Adomet_synth2; 1.
DR Pfam: PF02773; S-Adomet_synth3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
KW ATP-binding; Complete proteome: One-carbon metabolism; Transferase.
SQ SEQUENCE 399 AA; 43795 MW; 51C9A4DFCEAD5329 CRC64;

alignment_scores:

Quality: 61.00 Length: 18
Ratio: 4.067 Gaps: 0
Percent Similarity: 83.333 Percent Identity: 61.111

alignment_block:

US-09-198-779B-1 x Q9K7Q9 ..

Align seg 1/1 to: Q9K7Q9 from: 1 to: 399

169 AAGACCGCGCATACGCCACTTGGCCGTGACGACGCCGACTTCACCTG 218
:::|||||
370 GlnhtrAlaAlaIatYgLIhISphEGlyarGthrSasValGIuLeuProTr 386
219 CGAG 222
|||
386 pglu 387

seq_name: sp_bacteriap:Q92A25

seq_documentation_block:

ID Q92A25 PRELIMINARY; PRT; 399 AA.

AC Q92A25;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE METK PROTEIN.

GN METK OR LIN173.

OS Listeria innocua.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Listeria.

OX NCBI_TaxID=1642;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CLIP 11262 / SEROVAR 6A;

RX PubMed=11679669;

RA Glaser P., Franjeul L., Buchrieser C., Rusniok C., Amend A.,

RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,

RA Charbit A., Chehouani F., Couve E., de Darvar A., Dehoux P.,

RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurgey O.,

RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garido P.,

RA Gautier L., Goebel W., Gomez-Lopez N., Hahn T., Haut J., Jackson D.,

RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapat G.,

RA Madueno E., Maltounam A., Mata Vicente J., Ng E., Nedjari H.,

RA Nordstiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,

RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.,

RT "Comparative genomics of Listeria species.";

RL Science 294:849-852(2001).

DR EMBL; AL596169; CAC97004.1; -.

DR Listlist: LIN0173; -.

KW Complete proteome.

SQ SEQUENCE 399 AA; 43555 MW; 543905EDC51F3D90 CRC64;

alignment_scores:

Quality: 61.00 Length: 18
Ratio: 4.067 Gaps: 0
Percent Similarity: 83.333 Percent Identity: 61.111

alignment_block:

US-09-198-779B-1 x Q92A25 ..

Align seg 1/1 to: Q92A25 from: 1 to: 399

169 AAGACCGCGCATACGCCACTTGGCCGTGACGACGCCGACTTCACCTG 218
:::|||||
368 GlnhtrAlaAlaIatYgLIhISphEGlyarGthrSasValGIuLeuProTr 384
219 CGAG 222
|||
384 pglu 385

seq_name: sp_bacteriap:Q9KUP3

seq_documentation_block:

ID Q9KUP3 PRELIMINARY; PRT; 385 AA.

AC Q9KUP3;

DT 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE

GN METK OR VC0472.

OS Vibrio cholerae.

OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.

OX NCBI_TaxID=666;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=EL TOR N1661 / SEROTYPE O1;

RX MEDLINE=20406833; PubMed=10952301;

RA Heidelberg J.F., Eissen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,

RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

RA Gill S.R., Nelson K.E., Read T.D., Tetteijn H., Richardon D.,

RA Ermolaeva M.D., Yamathayan J., Bass S., Qin H., Dragoi I., Sellers P.,

RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,

RA Fraser C.M.;

RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*."

RL Nature 406:477-483(2000).

CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM METHIONINE AND ATP (BY SIMILARITY).

CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE + PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.

CC -1- PATHWAY: ACTIVATED METHYL CYCLE.

CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).

DR EMBL: AE004133; AAF93645.1; -.

DR HSSP: P04384; IMXB.

DR TIGR: VC0472; -.

DR InterPro: IPR002133; S-Adomet_synt.

DR Pfam: PF00438; S-Adomet_synt; 1.

DR Pfam: PF02772; S-Adomet_synt2; 1.

DR Pfam: PF02773; S-Adomet_synt3; 1.

DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.

DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.

KW ATP-binding; Complete proteome: One-carbon metabolism; Transferase.

SO SEQUENCE 385 AA; 4206 MW; D15C93B3C511FD86 CRC64;

alignment_scores:

Quality:	60.00	Length:	12
Ratio:	5.000	Gaps:	0
Percent Similarity:	100.000	Percent Identity:	83.333

alignment_block:

US-09-198-779B-1 x Q9KUP3 ..

Align seg 1/1 to: Q9KUP3 from: 1 to: 385

169 AAGACCGCCGATACGGCGACATGGCCGTCAGCAGC 204
|||||
355 LysThrAlaAlaArgLysGlyHisPheGlyArgGluGlu 366

seq_name: sp_archaeap:Q9HN07

seq_documentation_block:

ID Q9HN07 PRELIMINARY: PRT; 674 AA.

AC Q9HN07;

DT 01-MAR-2001 (TREMBLrel. 16, Created)

DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE ACYLAMINOACYL-PEPTIDASE.

GN YUXXL OR VNG2302G.

OS Halobacterium sp. (Strain NRC-1).

OC Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae; Halobacterium.

OC NCBI_TaxID=64091;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20504483; PubMed=11016950;

RA Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M., Shula H.D., Lasly S.R., Baliga N.S., Thorsson V., Strogonia J., Swartzell S., Weir D., Hall J., Dahl T.A., Welte R., Goo Y.A., Madocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isebnager T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alm M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;

RA "Genome sequence of Halobacterium species NRC-1."

RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).

DR EMBL: AE005114; AAG20414.1; -.

DR MEROPS: S09_UPC; -.

DR InterPro: IPR000379; Est_lip_thioest_actsite.

KW Complete proteome.

SO SEQUENCE 674 AA; 72577 MW; DDBEEF48896CCAV8 CRC64;

alignment_scores:

Quality: 60.00 Length: 87

Ratio: 1.579 Gaps: 3

Percent Similarity: 43.678 Percent Identity: 28.736

alignment_block:

US-09-198-779B-1/rev x Q9HN07 ..

Align seg 1/1 to: Q9HN07 from: 1 to: 674

228 GACCACCTCGCAGGTGAAGTCGGCGTCGTCAGCGCAAGTGGCCGATG 179
|||
183 AspleunlaalagLysArgValAspArgValThrIleGlyValAlaGly 199
178 CGGC.....
199 sGLyGLyProAlaArgpGLyAspArgpGLyThrLeuTyTyrProIleArg 216
174 ..GGTCTTGAT..... GAACCTGNNNNNNNNNNNNNNNNNN 142
|||
216 rGLyLeuAspAlaAspAspArgLeuGLyThrAlaIleGluAlaAlaThr 232
243ThrThrValGluGlyMetGlyProThrLeuAlaValH 255
41 ATGGCGACGCT 31
|||||
255 IsGLySerArg 258

seq_name: sp_invertebrate:Q9VEG7

seq_documentation_block:

ID Q9VEG7 PRELIMINARY: PRT; 2703 AA.

AC Q9VEG7;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE OSA PROTEIN.

GN OSA OR CG7467.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OC NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celinkner S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abriil J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borokov A.C., Botchan D.A., Bouck J., Brinkstein P., Brotlier P., Burlin K.C., Butam M.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dev I., Dietz S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Fertirel S., Fleischmann W., Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ileguam C., Jafaili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Moberly C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003718; AAF55457.1; -.
 DR FLYBase; FBgn0003013; osa.
 DR InterPro; IPR001606; ARID.
 DR InterPro; IPR002965; P_rich_extensn.
 DR Pfam; PF01388; ARID; 1.
 DR PRINTS; PR01217; PRICEXTNSN.
 DR SMART; SM00501; BRIGHT; 1.
 SQ SEQUENCE 2703 AA; 282894 MW; 27ED5BA0277A6369 CRC64;

alignment_scores: Quality: 60.00 Length: 22
 Ratio: 3.529 Gaps: 0
 Percent Similarity: 77.273 Percent Identity: 54.545

alignment block:

US-09-198-779B-1/rev x Q9VEG7 ..

Align seg 1/1 to: Q9VEG7 from: 1 to: 2703

```

84 AATAACACACGACGATGATCAGACCGCTCATTTATCAGCATGGGCA 35
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
46 AsnAsnAsnSerAsnAsnGlySerAspProSerIleGlnGlnGlnGlnI 62
   |:::  ::  |||
34 GCGTCGATCTGTCCAC 19
   |:::  ::  |||
62 nAsnValAlaProHis 67
  
```

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OM of: US-09-198-779B-1 to: SwissProt_40:* out_format : pfs
 Date: Aug 20, 2002 2:59 AM

About: Results were produced by the GenCore software, version 4.5,
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Command line parameters:

-MODEL-frame+ n2p model -DEV-x1p
 -O/cgn2_1/USPRO.spool/US09198779/runat_19082002.140913.25182/app-query.fasta.1.296
 -DB=SwissProt_40 -QEMT=fastan -SUFFIX=rs -GAPOP=12.000
 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPL=0.000 -LOOPEXT=0.000
 -OGAPOP=4.500 -OGAPEXT=0.050 -OGAPOP=10.000 -XGAPEXT=0.500
 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
 -DELPO=6.000 -DELEXT=7.000 -START=1 -MATRIX=blonum62
 -TRAS=human40 cdi -LIST=45 -DOCALLGN=200 -THR_SCORE=ptc
 -THR_MAX=100 -THR_MIN=0 -ALIGN=45 -MODE=LOCAL -OUTPRF=pts
 -NORW=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
 -USER=US09198779.ecgn1_1.23 -NCPU=6 -ICPU=3 -LONGLOG
 -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-198-779B-1
 Query length: 235
 Database: SwissProt_40:*
 Database sequences: 105224
 Database length: 3819550
 Search time (sec): 21.730000

score_list:

Sequence	Strid	Orig	ZScore	Escore	Len	i	Documentation
SwissProt_40:METK_HORVU	127	00	318.60	1.2e-10	394	1	P50299 hordeum vulgare (barl)
SwissProt_40:METK_ACTCH	125	00	313.96	2.4e-10	360	1	P50303 actinidia chinensis (c)
SwissProt_40:METK_MESCR	122	00	305.15	6.8e-10	392	1	P93254 mesembryanthemum crys
SwissProt_40:METK_ARATH	120	00	299.73	1.4e-09	393	1	P23686 arabidopsis thaliana
SwissProt_40:METK_BRAUJ	120	00	299.73	1.4e-09	393	1	P46611 brassica juncea (leaf
SwissProt_40:METK_CATRO	120	00	299.73	1.4e-09	393	1	P06551 catharanthus roseus (
SwissProt_40:METK_LYCES	120	00	299.73	1.4e-09	393	1	P43281 lycopersicon esculent
SwissProt_40:METK_POPDE	120	00	299.69	1.4e-09	395	1	P47916 populus deltoides (pc
SwissProt_40:METK_ORYSA	118	00	294.31	2.7e-09	394	1	P93438 oryza sativa (rice).
SwissProt_40:METK_MUSAC	117	00	291.64	3.8e-09	393	1	O22338 musa acuminata (banan
SwissProt_40:METK_ORYSA	117	00	291.57	3.8e-09	396	1	P46611 oryza sativa (rice).
SwissProt_40:METK_PETCR	116	00	297.29	5.0e-09	145	1	P31156 petroselinum crispum
SwissProt_40:METK_PETCR	116	00	293.28	5.2e-09	234	1	P31155 petroselinum crispum
SwissProt_40:METK_PEA	116	00	289.54	5.4e-09	366	1	P49612 pisum sativum (garden
SwissProt_40:METK_CATRO	116	00	288.94	5.4e-09	393	1	P06552 catharanthus roseus (
SwissProt_40:METL_ARATH	115	00	286.24	7.7e-09	393	1	P17562 arabidopsis thaliana
SwissProt_40:METK_PININ	103	00	253.86	4.9e-07	393	1	P50300 pinus banksiana (jack
SwissProt_40:METK_ACTCH	101	00	248.53	9.7e-07	390	1	P50301 actinidia chinensis (c)
SwissProt_40:METK_PETHY	101	00	248.53	9.7e-07	390	1	P47916 populus deltoides (pc
SwissProt_40:METL_LYCES	100	00	245.83	1.4e-06	390	1	P43281 lycopersicon esculent
SwissProt_40:METL_ACTCH	100	00	245.83	1.4e-06	390	1	P50302 actinidia chinensis (c)
SwissProt_40:METL_DIACA	98	00	240.31	2.8e-06	396	1	P24260 dianthus caryophyllus
SwissProt_40:METK_CATRO	87	00	210.75	0.0001	390	1	P06553 catharanthus roseus (
SwissProt_40:METK_RICTY	75	00	178.55	0.0079	382	1	O91199 rickettsia typhi. s.d
SwissProt_40:METK_RICPR	74	00	175.90	0.0111	380	1	P56878 rickettsia prowazeki
SwissProt_40:METK_THEMA	74	00	175.57	0.0111	395	1	O91198 thermotoga maritima
SwissProt_40:METK_ACACA	68	00	159.53	0.0888	388	1	O95032 acanthamoeba castella
SwissProt_40:METK_BACSV	65	00	151.18	0.2513	400	1	P54419 bacillus subtilis. s
SwissProt_40:METK_STRST	64	00	148.26	0.3559	411	1	O94492 streptomyces spectabi
SwissProt_40:METK_HUMAN	63	00	145.89	0.5016	395	1	P31155 homo sapiens (human)
SwissProt_40:METK_RAT	63	00	145.89	0.5016	395	1	P18288 rattus norvegicus (rat)
SwissProt_40:METK_MYCLE	63	00	145.72	0.5023	403	1	O9ecq4 mycobacterium lepreae
SwissProt_40:METK_HELPR	61	00	140.71	1.00	385	1	O9amns helicobacter pylori
SwissProt_40:METK_HELPR	61	00	140.71	1.00	385	1	P56605 helicobacter pylori
SwissProt_40:METK_STRAU	61	00	140.45	1.00	397	1	P50307 staphylococcus aureus
SwissProt_40:METK_BACHD	61	00	140.41	1.00	399	1	O9k7q9 bacillus halodurans.
SwissProt_40:METK_LACIA	61	00	140.41	1.00	399	1	O9ee07 lactococcus lactis (s
SwissProt_40:METK_MYCTV	61	00	140.33	1.00	403	1	P77899 mycobacterium tuberco
SwissProt_40:METK_SYNY3	60	50	138.51	1.20	426	1	P72871 synechocystis sp. (st

SwissProt_40:METK_TREPA + 59.00 135.08 2.00 396 | O83772 treponema pallidum
 SwissProt_40:METL_RAT + 59.00 135.06 2.00 397 | P13444 rattus norvegicus (r
 SwissProt_40:METK_BUCAT + 58.00 132.77 2.82 378 | P57486 buchnera aphidico
 SwissProt_40:POLN_SODV3 - 57.50 118.40 3.76 1788 | Q04544 southampton virus
 SwissProt_40:CLT2_HUMAN - 57.00 130.81 3.96 346 | Q9ns75 homo sapiens (hume

seq_name: SwissProt_40:METK_HORVU

seq_documentation_block:
 ID METK_HORVU STANDARD: PRT: 394 AA.

AC P50299;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE S-adenosylmethionine synthetase 1 (EC 2.5.1.6) (Methionine
 DE adenosyltransferase 1) (Adomet synthetase 1).
 GN SAM1.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OC NCBI_TaxId=4513;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mori S., Takizawa R.,
 RN Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RP TISSUE=Root;
 RA Mori S., Takizawa R., Nakanishi H.;
 RN Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
 CC METHIONINE AND ATP.
 CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
 CC diphosphate + S-adenosyl-L-methionine.
 CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
 CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

CC EMBL: D63835; BAA09895.1; -;
 CC EMBL: D49655; BAA08531.1; -;
 CC DR HSSP: P04384; IMXB.
 CC DR InterPro: IPR002133; S-Adomet-synt.
 CC DR Pfam: PF00438; S-Adomet-synt. 1.
 CC DR Pfam: PF02772; S-Adomet-syntD2; 1.
 CC DR Pfam: PF02773; S-Adomet-syntD3; 1.
 CC DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
 CC DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
 CC KW Transfease; One-carbon metabolism; Multigene family; ATP-binding.
 CC FT NP BIND 121 126 ATP (POTENTIAL).
 CC FT BINDING 149 149 ATP (POTENTIAL).
 CC SQ SEQUENCE 394 AA: 42841 MW: 2ED786F33530013 CRC64;

alignment_scores:

Quality: 127.00 Length: 25
 Ratio: 5.292 Gaps: 0
 Percent Similarity: 96.000 Percent Identity: 96.000

alignment_block:

US-09-198-779B-1 x METK_HORVU ..

Align seg 1/1 to: METK_HORVU from: 1 to: 394

160 AGGTTTCATCAAGACCGCCGATACGGCCATTGGCCGTGACGACGCCGA 209
 |||

362 ArgpHeilelysthrAlaIaIaTyrglyHisPheGlyArgAspAlaAs 378
210 CTTCACTTCAGAGCCGCGATAGCGCCACTTTGGCCGTACGAGCGCA 234
||||| |||||||
378 pPheHTrTPGluValValLysPro 386

seq_name: SwissProt_40:METM_ACTCH

seq_documentation_block:

ID METM_ACTCH STANDARD; PRT; 360 AA.
AC P50303;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE S-adenosylmethionine synthetase 3 (EC 2.5.1.6) (Methionine
adenosyltransferase 3) (Adomet synthetase 3) (Fragment).
OS Actinidia chinensis (Kiwi) (Actinidia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Ericales; Actinidiaceae; Actinidia.
OX NCBI_Taxid=3625;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95357424; PubMed=7630953;
RA Wiltaker D.J., Smith G.S., Gardner R.C.;
RT "Three cDNAs encoding S-adenosyl-L-methionine synthetase from
Actinidia chinensis".
RL Plant Physiol. 108:1307-1308(1995).
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
METHIONINE AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
diphosphate + S-adenosyl-L-methionine.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
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or send an email to license@isb-sib.ch).
CC
CC EMBL: U17241; AAA81379.1; -
DR HSSP: P04384; IMXB.
DR InterPro: IPR002133; S-Adomet_synt.
DR Pfam: PF00438; S-Adomet_synt.1.
DR Pfam: PF02772; S-Adomet_synt2; 1.
DR Pfam: PF02773; S-Adomet_synt3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
KW Transferase; One-carbon metabolism; Multigene family; ATP-binding.
FT NON_TER 1 1
FT NP_BIND 86 91 ATP (POTENTIAL).
FT BINDING 114 114 ATP (POTENTIAL).
SQ SEQUENCE 360 AA; 39513 MW; E8B2626FE6E71171 CRC64;

alignment_scores:

Quality: 125.00 Length: 25
Ratio: 5.208 Gaps: 0
Percent Similarity: 96.000 Percent Identity: 92.000

alignment_block:

US-09-198-779b-1 x METM_ACTCH ..

Align seg 1/1 to: METM_ACTCH from: 1 to: 360

160 AGGTTTCATCAAGACCGCGCATAGCGCCACTTTGGCCGTACGAGCGCA 209
|||||:|||||
328 ArgPheIeuLysThrAlaIaIaTyrglyHisPheGlyArgAspAlaAs 344
210 CTTCACTTCAGAGCCGCGATAGCGCCACTTTGGCCGTACGAGCGCA 234

||||| |||||||
344 pPheHTrTPGluValValLysPro 352

seq_name: SwissProt_40:METK_MESCR

seq_documentation_block:

ID METK_MESCR STANDARD; PRT; 392 AA.
AC P93254;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE S-adenosylmethionine synthetase 4 (EC 2.5.1.6) (Methionine
adenosyltransferase) (Adomet synthetase).
OS Mesembryanthemum crystallinum (Common ice plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllales; Alzooceae; Mesembryanthemum.
OX NCBI_Taxid=3544;
RN [1]
RP SEQUENCE FROM N.A.
RA Michalowski C.B., Bohnert H.J.;
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
METHIONINE AND ATP (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
diphosphate + S-adenosyl-L-methionine.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
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or send an email to license@isb-sib.ch).
CC
CC EMBL: U79767; AAB38500.1; -
DR HSSP: P04384; IMXB.
DR InterPro: IPR002133; S-Adomet_synt.
DR Pfam: PF00438; S-Adomet_synt.1.
DR Pfam: PF02772; S-Adomet_synt2; 1.
DR Pfam: PF02773; S-Adomet_synt3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
KW Transferase; One-carbon metabolism; Multigene family; ATP-binding.
FT NP_BIND 119 124 ATP (POTENTIAL).
FT BINDING 147 147 ATP (POTENTIAL).
SQ SEQUENCE 392 AA; 42885 MW; D13C2CD03757165A CRC64;

alignment_scores:

Quality: 122.00 Length: 25
Ratio: 5.083 Gaps: 0
Percent Similarity: 96.000 Percent Identity: 88.000

alignment_block:

US-09-198-779b-1 x METK_MESCR ..

Align seg 1/1 to: METK_MESCR from: 1 to: 392

160 AGGTTTCATCAAGACCGCGCATAGCGCCACTTTGGCCGTACGAGCGCA 209
|||||:|||||
360 ArgTyrlEuLysThrAlaIaIaTyrglyHisPheGlyArgAspAlaAs 376

210 CTTCACTTCAGAGCCGCGATAGCGCCACTTTGGCCGTACGAGCGCA 234
||||| |||||||

376 pPheHTrTPGluValValLysPro 384

seq_name: SwissProt_40:METK_ARATH

seq_documentation_block:

ID METK_ARATH STANDARD; PRT; 393 AA.

AC P23686;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1991 (Rel. 20, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE S-adenosylmethionine synthetase 1 (EC 2.5.1.6) (Methionine
 DE adenosyltransferase 1) (Adomet synthetase 1).
 GN SAM1.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92386056; PubMed=2535470;
 RA Peleman J., Boerjan W., Engler G., Seurinck J., Botterman J.,
 RA Alliotte T., van Montagu M., Inze D.;
 RT "Strong cellular preference in the expression of a housekeeping gene
 RT of Arabidopsis thaliana encoding S-adenosylmethionine synthetase.";
 RL Plant Cell 1:81-93(1989).
 RN [2]
 RP SEQUENCE OF 1-116 AND 363-393 FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Reynal M., Grellet F., Laudie M., Meyer Y., Cooke R., Delseny M.;
 RL Submitted (OCT-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
 CC METHIONINE AND ATP.
 CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
 CC diphosphate + S-adenosyl-L-methionine.
 CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
 CC -1- MISCELLANEOUS: IN A.THALIANA, THERE ARE TWO GENES ENCODING THIS
 CC PROTEIN (SAM1 AND SAM2).
 CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: M55077; AAA32868.1; -;
 DR EMBL: Z17672; CAA79031.1; -;
 DR EMBL: Z17762; CAA79057.1; -;
 DR PIR: JN0131; JN0131.
 DR HSP: P04384; IMXB.
 DR InterPro: IPR002133; S-Adomet_synt.
 DR Pfam: PF00438; S-Adomet_synt.1.
 DR Pfam: PF02772; S-Adomet_synt2; 1.
 DR Pfam: PF02773; S-Adomet_synt3; 1.
 DR PROSITE: PS00376; ADOMET_SYNTHETASE.1; 1.
 DR PROSITE: PS00377; ADOMET_SYNTHETASE.2; 1.
 DR TRANSFERASE: One-carbon metabolism; Multigene family; ATP-binding.
 KW NP_BIND 119 124 ATP (POTENTIAL).
 FT BINDING 147 147 ATP (POTENTIAL).
 FT BINDING 147 147
 SO SEQUENCE 393 AA; 43144 MW; 270BA43AF52D4543 CRC64;

Alignment_scores:
 Quality: 120.00 Length: 25
 Ratio: 5.217 Gaps: 0
 Percent Similarity: 92.000 Percent Identity: 88.000

Alignment_block:

US-09-198-779b-1 x METK_ARATH ..

Align seg 1/1 to: METK_ARATH from: 1 to: 393

160 AGGTCATCAAGAGCGCGCATAGCGCACTTGGCCGAGAGAGCGCA 209
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 361 ArgPheLeuLysThrAlaIatYrGlYhSpNegIYArgAspAspProAs 377

210 CTTCACTGCGAGGTGTCAAGCCC 234
 |||||:|||||:|||||:|||||:|||||:|||||:|||||
 377 PetherTrpGluValValLysPro 385

seq_name: SwissProt_40:METK_BRAJU

seq_documentation_block:

ID METK_BRAJU STANDARD; PRT; 393 AA.
 AC P49611;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine
 DE adenosyltransferase) (Adomet synthetase).
 GN SAM5.
 OS Brassica juncea (Leaf mustard) (Indian mustard).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Brassicae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3707;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. INDIA MUSTARD; TISSUE=Leaf;
 RX MEDLINE=95232187; PubMed=7716233;
 RA Wen C.M., Wu M., Goh C.J., Pua E.C.;
 RT "Cloning and nucleotide sequence of a cDNA encoding S-adenosyl-L-
 RT methionine synthetase from mustard (Brassica juncea [L.] Czern &
 RT Coss).";
 RL Plant Physiol. 107:1021-1022(1995).
 CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
 CC METHIONINE AND ATP.
 CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
 CC diphosphate + S-adenosyl-L-methionine.
 CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
 CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X80362; CAA56590.1; -;
 DR HSP: P04384; IMXB.
 DR InterPro: IPR002133; S-Adomet_synt.
 DR Pfam: PF00438; S-Adomet_synt.1.
 DR Pfam: PF02772; S-Adomet_synt2; 1.
 DR Pfam: PF02773; S-Adomet_synt3; 1.
 DR PROSITE: PS00376; ADOMET_SYNTHETASE.1; 1.
 DR PROSITE: PS00377; ADOMET_SYNTHETASE.2; 1.
 DR TRANSFERASE: One-carbon metabolism; Multigene family; ATP-binding.
 KW NP_BIND 119 124 ATP (POTENTIAL).
 FT BINDING 147 147 ATP (POTENTIAL).
 FT BINDING 147 147
 SO SEQUENCE 393 AA; 43326 MW; 50188D87C5EB41PA CRC64;

Alignment_scores:
 Quality: 120.00 Length: 25
 Ratio: 5.217 Gaps: 0
 Percent Similarity: 92.000 Percent Identity: 88.000

Alignment_block:

US-09-198-779b-1 x METK_BRAJU ..

Align seg 1/1 to: METK_BRAJU from: 1 to: 393

160 AGGTCATCAAGAGCGCGCATAGCGCACTTGGCCGAGAGAGCGCA 209
 |||||:|||||:|||||:|||||:|||||:|||||:|||||
 361 ArgPheLeuLysThrAlaIatYrGlYhSpNegIYArgAspAspProAs 377
 210 CTTCACTGCGAGGTGTCAAGCCC 234

|||||
377 pphenrttrpglvalvalyspro 385

seq_name: SwissProt_40:METK_CATRO

seq_documentation_block:

ID METK_CATRO STANDARD: PRT: 393 AA.

AC O96551;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DE 15-JUL-1998 (Rel. 36, Last annotation update)

DE S-adenosylmethionine synthetase 1 (EC 2.5.1.6) (Methionine

adenosyltransferase 1) (Adomet synthetase 1).

GN SAMSL.

OS Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfiaceae;

OC Viscaceae; Catharanthus.

NCBI_TaxID=4058;

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seq_name: SwissProt_40:METK_LYCES

seq_documentation_block:

ID METK_LYCES STANDARD: PRT: 393 AA.

AC P43280;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DE S-adenosylmethionine synthetase 1 (EC 2.5.1.6) (Methionine

adenosyltransferase 1) (Adomet synthetase 1).

GN SAMSL.

OS Lycopersicon esculentum (Tomato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

NCBI_TaxID=4081;

OR

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seq_name: SwissProt_40:METL_LYCES

seq_documentation_block:

ID METL_LYCES STANDARD: PRT: 393 AA.

AC P43280;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DE S-adenosylmethionine synthetase 1 (EC 2.5.1.6) (Methionine

adenosyltransferase 1) (Adomet synthetase 1).

GN SAMSL.

OS Lycopersicon esculentum (Tomato).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

NCBI_TaxID=4081;

OR

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DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE S-adenosylmethionine synthetase 2 (EC 2.5.1.6) (methionine
GN SAM2 OR SAM52.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eubacteriales; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim W.T.
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP (BY SIMILARITY).
CC -! CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -! PATHWAY: ACTIVATED METHYL CYCLE.
CC -! SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U82833; AAC05590.1; -.
DR HSSP: P04384; 1MXB.
DR AND-2PAGE; P93438; -.
DR InterPro: IPR002133; S-Adomet_synth.
DR Pfam: PF00438; S-Adomet_synth.1.
DR Pfam: PF02772; S-Adomet_synthD3.1.
DR Pfam: PF02773; S-Adomet_synthD3.1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
DR TRANSFERASE; One-carbon metabolism; Multigene family; ATP-binding.
FT NP_BIND 121 126 ATP (POTENTIAL).
FT BINDING 149 149 ATP (POTENTIAL).
FT SEQUENCE 394 AA; 42900 MW; 081E9F3B65694EB7 CRC64;

alignment_scores:
Quality: 118.00 Length: 25
Ratio: 5.130 Gaps: 0
Percent Similarity: 92.000 Percent Identity: 88.000

alignment_block:
US-09-198-779b-1 x METL_ORYSA ..
Align seg 1/1 to: METL_ORYSA from: 1 to: 394

160 AGGTTCAATCAAGACCGCGCATAGCGCCACTTTGGCCGTGACGACGCCGA 209
|||||
362 ArgthelleystrhalaalaatyrglyhlsphelgylargslusprroAs 378
210 CTTACACCTGCGAGGTGTCAGCCC 234
|||||
378 phethtrtpgluvalvalyspro 386

seq_name: Swissprot_40:METK_MUSAC

seq_documentation_block:
ID METK_MUSAC STANDARD: PRT: 393 AA.
AC 022338:
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (methionine
DE adenosyltransferase) (Adomet synthetase).
OS Musa acuminata (Banana).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

```

OC Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
OC Musa.
OX NCBI_TaxID=4641;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-CV. HSIEH JIN CHIAO: TISSUE-Fruit;
RA Do Y.-Y., Chang C.-Y., Cheng C.-F., Huang P.-L.;
RT "Cloning and nucleotide sequence of a S-adenosyl-L-methionine
RT synthetase cDNA from banana."
CC (in) Plant Gene Register PGR97-101.
CC -! FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP.
CC -! CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -! PATHWAY: ACTIVATED METHYL CYCLE.
CC -! SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF004317; AAB71138.1; -.
DR HSSP: P04384; 1MXB.
DR InterPro: IPR002133; S-Adomet_synth.
DR Pfam: PF00438; S-Adomet_synth.1.
DR Pfam: PF02772; S-Adomet_synthD3.1.
DR Pfam: PF02773; S-Adomet_synthD3.1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
DR TRANSFERASE; One-carbon metabolism; Multigene family; ATP-binding.
FT NP_BIND 120 125 ATP (POTENTIAL).
FT BINDING 148 148 ATP (POTENTIAL).
FT SEQUENCE 393 AA; 43151 MW; 259FB121A49B8591 CRC64;

alignment_scores:
Quality: 117.00 Length: 25
Ratio: 5.087 Gaps: 0
Percent Similarity: 92.000 Percent Identity: 84.000

alignment_block:
US-09-198-779b-1 x METK_MUSAC ..
Align seg 1/1 to: METK_MUSAC from: 1 to: 393

160 AGGTTCAATCAAGACCGCGCATAGCGCCACTTTGGCCGTGACGACGCCGA 209
|||||
361 ArgtylleuylstrhalaalaatyrglyhlsphelgylargslusprroAs 377
210 CTTACACCTGCGAGGTGTCAGCCC 234
|||||
377 phethtrtpgluvalvalyspro 385

seq_name: Swissprot_40:METK_ORYSA

seq_documentation_block:
ID METK_ORYSA STANDARD: PRT: 396 AA.
AC P46611:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE S-adenosylmethionine synthetase 1 (EC 2.5.1.6) (methionine
DE adenosyltransferase 1) (Adomet synthetase 1).
GN SAM1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eubacteriales; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. TAICHUNG.
RX MEDLINE=95062735; PubMed=7972513;
RA van Breusegem F., Dekeyser R., Gielens J., van Montagu M.,
RT "Characterization of a S-adenosylmethionine synthetase gene in rice.";
RL Plant Physiol. 105:1463-1464(1994).
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z26867; CA81481.1; -.
DR HSSP; P04384; IMXB.
DR ANU-2DPAGE; P46611; -.
DR InterPro: IPR002133; S-Adomet_synth.
DR Pfam; PF00438; S-Adomet_synth; 1.
DR Pfam; PF02772; S-Adomet_synth2; 1.
DR Pfam; PF02773; S-Adomet_synth3; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
KM Transferrase; One-carbon metabolism; Multigene family; ATP-binding.
FT BINDING 122 127 ATP (POTENTIAL).
FT BINDING 150 150 ATP (POTENTIAL).
SQ SEQUENCE 396 AA; 43220 MW; 16FE43474045FEB9 CRC64;

alignment_scores:
    Quality: 117.00      Length: 25
    Ratio: 5.087        Gaps: 0
    Percent Similarity: 92.000      Percent Identity: 84.000

alignment_block:
US-09-198-779B-1 x METK_ORYSA  ..
Align seg 1/1 to: METK_ORYSA from: 1 to: 396

160 AGGTTTCATCAAGACCGCGCATACGCGCATTGGCCGTGACGACGCCGA 209
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
364 ArgTyrLeuLysThrAlaIatYrGlyHisPheGlyArgGAspAspProAs 380
210 CTTCACTCGCAGGCGTGTCAAGCCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
380 pPheThrTrpGluValValLysPro 388

seq_name: SwissProt_40:METL_PETCR

seq_documentation_block:
ID METL_PETCR STANDARD; PRT; 145 AA.
AC P31156;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE S-adenosylmethionine synthetase 2 (EC 2.5.1.6) (Methionine
DE adenosyltransferase 2) (Adomet synthetase 2) (Fragment).
GN SMS-2.
OS Petroselinum crispum (Parsley) (Petroselinum hortense).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Apiales; Apiaceae; Petroselinum.
OX NCBI_TaxID=4043;
RN [1]
RP SEQUENCE FROM N.A.

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RP SEQUENCE FROM N.A.
RC TISSUE=leaf;
RX MEDLINE=92262510; PubMed=1374911;
RA Kwallieck P., Plesch G., Hahnbrock K., Somssich I.E.;
RT "Induction by fungal elicitor of S-adenosyl-L-methionine synthetase
RT and S-adenosyl-L-homocysteine hydrolyase mRNAs in cultured cells and
RL leaves of Petroselinum crispum.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4713-4717(1992).
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- TISSUE SPECIFICITY: MAINLY IN FLORAL BUDS AND ROOTS.
CC -1- INDUCTION: BY FUNGAL ELICITOR.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M62757; AAA33858.1; -.
DR HSSP; P04384; IMXB.
DR InterPro: IPR002133; S-Adomet_synth.
DR Pfam; PF00438; S-Adomet_synth; 1.
DR Pfam; PF02773; S-Adomet_synth3; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; PARTIAL.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
KM Transferrase; One-carbon metabolism; Multigene family; ATP-binding.
FT BINDING 1 1
FT BINDING 145 AA; 15758 MW; 900FEB6A472EB08 CRC64;
SQ SEQUENCE 145 AA; 15758 MW; 900FEB6A472EB08 CRC64;

alignment_scores:
    Quality: 116.00      Length: 25
    Ratio: 5.043        Gaps: 0
    Percent Similarity: 92.000      Percent Identity: 84.000

alignment_block:
US-09-198-779B-1 x METL_PETCR  ..
Align seg 1/1 to: METL_PETCR from: 1 to: 145

160 AGGTTTCATCAAGACCGCGCATACGCGCATTGGCCGTGACGACGCCGA 209
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
115 ArgPheLeuLysThrAlaIatYrGlyHisPheGlyArgGluAspProAs 131
210 CTTCACTCGCAGGCGTGTCAAGCCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
131 pPheThrTrpGluValValLysPro 139

seq_name: SwissProt_40:METK_PETCR

seq_documentation_block:
ID METK_PETCR STANDARD; PRT; 234 AA.
AC P31155;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE S-adenosylmethionine synthetase 1 (EC 2.5.1.6) (Methionine
DE adenosyltransferase 1) (Adomet synthetase 1) (Fragment).
GN SMS-1.
OS Petroselinum crispum (Parsley) (Petroselinum hortense).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids II; Apiales; Apiaceae; Petroselinum.
OX NCBI_TaxID=4043;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Leaf;
RX MEDLINE=92262510; PubMed=1374911;
RA Kawalleck P., Plesch G., Hahlbrock K., Somsich I.E.:
RT "Induction by fungal elicitor of S-adenosyl-L-methionine synthetase
RT and S-adenosyl-L-homocysteine hydrolase mRNAs in cultured cells and
RT leaves of Petroselinum crispum."
RL Proc. Natl. Acad. Sci. U.S.A. 89:4713-4717(1992).
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- TISSUE SPECIFICITY: MAINTX IN FLORAL BUDS AND ROOTS.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M62758; AAA33857.1; -.
DR HSSP; P04384; IMXB.
DR InterPro: IPR002133; S-Adomet_synth.
DR Pfam; PF00438; S-Adomet_synth2; 1.
DR Pfam; PF02772; S-Adomet_synth2; 1.
DR Pfam; PF02773; S-Adomet_synth3; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; PARTIAL.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
KW Transferase; One-carbon metabolism; Multigene family; ATP-binding.
FT NON_TER 1
FT BINDING 1
SQ SEQUENCE 234 AA; 25652 MW; 8491086FA5D16BDA CRC64;

alignment_scores:
Quality: 116.00 Length: 25
Ratio: 5.043 Gaps: 0
Percent Similarity: 92.000 Percent Identity: 84.000

alignment_block:
US-09-198-779B-1 x METK_PETCR ..
Align seg 1/1 to: METK_PETCR from: 1 to: 234

160 AGGTTTCATCAAGACCGCCGATACGGCCACTTTGGCCGTGACGAGCCGA 209
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
204 ArpPheLeuYstHrAlaAlaIatYrGlyHisPheGlyArgGluAspProAs 220
210 CTTACCTGCGAGGTGTCAGCCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
220 pPheHTrpGluValValLysPro 228

seq_name: SwissProt_40:METK_PEA

seq_documentation_block:
ID METK_PEA STANDARD; PRT; 366 AA.
AC P49612;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE S-adenosylmethionine synthetase 1 (EC 2.5.1.6) (Methionine
DE adenosyltransferase 1) (Adomet synthetase 1) (Fragment).
GN SAMS1.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RP SEQUENCE FROM N.A.
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```
RC STRAIN=CV ALASKA;
RX MEDLINE=96194463; PubMed=8624412;
RA Gomez L., Carrasco P.:
RT "Hormonal regulation of S-adenosylmethionine synthase transcripts in
RT pea ovaries."
RL Plant Mol. Biol. 30:821-832(1996).
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; X82076; CAA57580.1; -.
DR EMBL; L36680; AAA58772.1; ALT_SEQ.
DR HSSP; P04384; IMXB.
DR InterPro: IPR002133; S-Adomet_synth.
DR Pfam; PF00438; S-Adomet_synth; 1.
DR Pfam; PF02772; S-Adomet_synth2; 1.
DR Pfam; PF02773; S-Adomet_synth3; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
KW Transferase; One-carbon metabolism; Multigene family; ATP-binding.
FT NON_TER 1
FT BINDING 1
FT NE_BIND 94
FT BINDING 122
FT BINDING 122
SQ SEQUENCE 366 AA; 39939 MW; EDB446F5D407627 CRC64;

alignment_scores:
Quality: 116.00 Length: 25
Ratio: 5.043 Gaps: 0
Percent Similarity: 92.000 Percent Identity: 84.000

alignment_block:
US-09-198-779B-1 x METK_PEA ..
Align seg 1/1 to: METK_PEA from: 1 to: 366

160 AGGTTTCATCAAGACCGCCGATACGGCCACTTTGGCCGTGACGAGCCGA 209
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
336 ArpPheLeuYstHrAlaAlaIatYrGlyHisPheGlyArgGluAspProAs 352
210 CTTACCTGCGAGGTGTCAGCCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
352 pPheHTrpGluValValLysPro 360

seq_name: SwissProt_40:METL_CATRO

seq_documentation_block:
ID METL_CATRO STANDARD; PRT; 393 AA.
AC Q96552;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE S-adenosylmethionine synthetase 2 (EC 2.5.1.6) (Methionine
DE adenosyltransferase 2) (Adomet synthetase 2).
GN SAMS2.
OS Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Gentianales; Apocynaceae; Rauvolfioideae;
OC Viscaceae; Catharanthus.
OX NCBI_TaxID=4058;
RN [1]
RP SEQUENCE FROM N.A.
```

RA Peleman , Saito K., Cottlyn B., Engler G., Seurinck J.,
RA van Montagu M., Inze D.;
RT "Structure and expression analyses of the S-adenosylmethionine
RT synthetase gene family in Arabidopsis thaliana.";
RL Gene 84:359-369(1989).
RP [2]
RN SEQUENCE FROM N.A.
RC STRAIN-CV, COLUMBIA;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Schueller C., Wambitt R., Murphy G., Volckaert G.,
RA Pohl T., Duetschhoeft A., Stiekema W., Entian K.-D., Terryn N.,
RA Harris B., Ansojge W., Brandt P., Griwell L.A., Rieger M.,
RA Weichselgartner M., de Simone V., Obermaier B., Maché R., Mueller M.,
RA Kreis W., Deisenhofer M., Puigdomenech P., Watson M., Schmidtheini F.,
RA Reichert B., Pottelette D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hohelselt J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Blahm L., Robben J.,
RA Van der Schueren J., Gymnoprez B., Chung Y.-J., Vandebussche F.,
RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Detorpe E.,
RA Weltzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA Holzner E., Brandt A., Peters S., van Staveren M., Dirke W.,
RA Moiljaner P., Klein Lanthorst R., Rose M., Hauf J., Koetter P.,
RA Benescher S., Hempel S., Feldpausch M., Lambrecht S., Van den Daele H.,
RA De Keyser A., Buyschaert C., Gielen J., Villarroel S., De Clercq R.,
RA Van Montgu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay M., Leonard N., McKay K., Mayes R.,
RA Petlett A., Rajadream M.A., Lyne M., Benes V., Rechmann S.,
RA Borczyk D., Blocker H., Scharfe M., Grimm M., Loehart T.-H.,
RA Dose S., de Haan M., Mease A.C., Schaefter M., Mueller-Auer S.,
RA Gabell C., Fuchs M., Fatmann B., Grandjean K., Dauner D., Herzl A.,
RA Neumann C., Argirion A., Vitale D., Ligouri R., Piravandi E.,
RA Massenet O., Outgley F., Clabaud G., Muendlein A., Felber R.,
RA Schmal S., Hiller R., Schmidt W., Lecharny A., Aboung S.,
RA Chedof F., Cooke R., Berger C., Monfort A., Cascuberta E.,
RA Gibbons T., Weber N., Vandenpol M., Baquies M., Terol J., Torres A.,
RA Perez-Perez A., Punelle B., Bent E., Johnson S., Taon D., Jesse T.,
RA Heijnen L., Schwarz S., Scholler P., Heber S., Frances P., Bieler C.,
RA Frisman D., Haese D., Lemcke K., Kewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA Panell L., Dedila N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threidel J.,
RA Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA Nelson J., Splich J., Ryan E., Andrews S., Geisel C., Layman D.,
RA Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshi C.,
RA Antoniou B., Zitanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA Swaby I.R., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA Granat S., Shohay N., Hasegawa A., Hamed A., Lodhi M., Johnson A.,
RA Chen E., Marra M., Martienssen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana."
RT Nature 402:769-777(1999).
RP [3]
RN SEQUENCE OF 141-248 AND 322-393 FROM N.A.
RC STRAIN-CV, COLUMBIA; TISSUE=seedling;
RX MEDLINE=20083488; PubMed=10617198;
RA Desprez T., Amselem J., Chiapello H., Caboche M., Hotte H.;
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2O) = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- MISCELLANEOUS: IN A.THALIANA, THERE ARE TWO GENES ENCODING THIS
CC PROTEIN (SAM1 AND SAM2).
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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DR EMBL; M33217; AAA32869.1; -
DR EMBL; AC007138; AAD22647.1; -
DR EMBL; AL161493; CAB80678.1; -
DR EMBL; Z33778; CAAB3930.1; -
DR EMBL; Z29136; CAAB3933.1; -
DR PIR; J00410; J00410.
DR HSSP; P04384; IMXB.
DR InterPro; IPR002133; S-AdoMet_synth.
DR Pfam; PF00438; S-AdoMet_synth; 1.
DR Pfam; PF02772; S-AdoMet_synth2; 1.
DR Pfam; PF02773; S-AdoMet_synth3; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
DR Transferase; One-carbon metabolism; Multigene family; ATP-binding.
FT NP_BIND 119 124 ATP (POTENTIAL).
FT BINDING 147 147 ATP (POTENTIAL).
SQ SEQUENCE 393 AA; 43255 MW; CE008EA565FD1FBC CRC64;

alignment_scores:
Quality: 115.00 Length: 25
Ratio: 5.227 Gaps: 0
Percent Similarity: 88.000 Percent Identity: 88.000

alignment_block:
US-09-198-779B-1 x METL_ARATH ..
Align seg 1/1 to: METL_ARATH from: 1 to: 393

160 AGGTCATCAGACCGCGCATACGGCCACTTTGGCCGTGACGACGCCGA 209
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||
361 ArgPheGlnLysThrAlaAlaIleTyrGlyHisPheGlyArgAspAspProAs 377
210 CTCGACCTGCGAGGTGTCAGCCC 234
||||| ||||||| ||||||| ||||||| ||||||| ||
377 pPheThrTrpGluValValValysPro 385

seq_name: SwissProt_40:METK_P1NBN

seq_documentation_block:
ID METK_P1NBN STANDARD; PRT; 393 AA.
AC P50300;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine
adenosyltransferase) (AdoMet synthetase).
OS Pinus banksiana (Jack pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3335;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Root;
RA Mayne M.B., Coleman J.R., Blumwald E.;
RL Submitted (OCT-1995) to the EMBL/Genbank/DBJ databases.
CC - FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP.
CC - CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC - PATHWAY: ACTIVATED METHYL CYCLE.
CC - TISSUE SPECIFICITY: ROOT.
CC - SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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DR EMBL; U38186; AA879831.1; -
DR HSSP; P04384; IMXB.
DR InterPro; IPR002133; S-AdoMet_synth.
DR Pfam; PF00438; S-AdoMet_synth; 1.
DR Pfam; PF02772; S-AdoMet_synth2; 1.
DR Pfam; PF02773; S-AdoMet_synth3; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
DR Transferase; One-carbon metabolism; Multigene family; ATP-binding.
FT NP_BIND 119 124 ATP (POTENTIAL).
FT BINDING 147 147 ATP (POTENTIAL).
SQ SEQUENCE 393 AA; 43168 MW; D12F7BP9B634185E CRC64;

alignment_scores:
Quality: 103.00 Length: 22
Ratio: 5.150 Gaps: 0
Percent Similarity: 90.909 Percent Identity: 86.364

alignment_block:
US-09-198-779B-1 x METK_P1NBN ..
Align seg 1/1 to: METK_P1NBN from: 1 to: 393

169 AAGACCGCCGCATACGGCCACTTTGGCCGTGACGACGCCGACTTCACCTG 218
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364 LysThrAlaIleTyrGlyHisPheGlyArgAspAspProAspPheThr 380
219 CGAGGTGTCAGCCC 234
||||| ||||||| ||||||| ||||||| ||||||| ||
380 pGluThrValValysPro 385

seq_name: SwissProt_40:METK_ACTCH

seq_documentation_block:
ID METK_ACTCH STANDARD; PRT; 390 AA.
AC P50301;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE S-adenosylmethionine synthetase 1 (EC 2.5.1.6) (Methionine
adenosyltransferase 1) (AdoMet synthetase 1).
OS Actinidia chinensis (Kiwi) (Yangtiao).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asterales; Ericales; Actinidiaceae; Actinidia.
OX NCBI_TaxID=3625;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95357424; PubMed=7630953;
RA Whitaker D.J., Smith G.S., Gardner R.C.;
RL "Three cDNAs encoding S-adenosyl-L-methionine synthetase from
RT Actinidia chinensis".
RL Plant Physiol. 108:1307-1308(1995).
CC - FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP.
CC - CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC - PATHWAY: ACTIVATED METHYL CYCLE.
CC - SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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DR EMBL; U17240; AAA81378.1; -

DR HSSP: P04384; 1MXB.
 DR InterPro: IPR002133; S-Adomet_synt.
 DR Pfam: PF00438; S-Adomet_synt; 1.
 DR Pfam: PF02773; S-Adomet_synt2; 1.
 DR Pfam: PF02773; S-Adomet_synt3; 1.
 DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
 DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
 DR TRANSFERASE: One-carbon metabolism; Multigene family; ATP-binding.
 FT BINDING 119 124 ATP (POTENTIAL).
 FT BINDING 147 147 ATP (POTENTIAL).
 SQ SEQUENCE 390 AA; 42519 MW; E3B6B10112B1E31 CRC64;

alignment_scores:
 Quality: 101.00 Length: 24
 Ratio: 4.810 Gaps: 0
 Percent Similarity: 87.500 Percent Identity: 79.167

alignment_block:
 US-09-198-779B-1 x METK_ACTCH ..

Align seg 1/1 to: METK_PETHY from: 1 to: 390

160 AGGTTTCATCAGACCGCGCATACGCCACTTGGCCGTGACGACGCCGA 209
 |||::: |||||
 361 ArgTyrGlnLysThrAlaIatYrGlyHisPheGlyArgAspAspProAs 377
 210 CTCACCTGCGAGGTGTCAG 231
 ||||| |||::: |||||
 377 pPheThrTrpGlnThrValLys 384

seq_name: SwissProt_40:METK_PETHY

seq_documentation_block:
 ID METK_PETHY STANDARD: PRT; 390 AA.
 AC P48498;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine
 adenosyltransferase) (Adomet synthetase).
 GN SAM1.
 OS Petunia hybrida (Petunia).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
 OX NCBI_TaxID=4102;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. V-26; TISSUE=Corolla;
 RX MEDLINE=95334508; PubMed=7610179;
 RA Izhaki A., Shoseyov O., Weiss D.;
 RT Plant Physiol. 108:841-842(1995).
 RL
 CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
 CC METHIONINE AND ATP.
 CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
 CC diphosphate + S-adenosyl-L-methionine.
 CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
 CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: X82214; CAA57696.1; -
 DR HSSP: P04384; 1MXB.
 DR InterPro: IPR002133; S-Adomet_synt.
 DR Pfam: PF00438; S-Adomet_synt; 1.
 DR Pfam: PF02773; S-Adomet_synt2; 1.

DR Pfam: PF02772; S-Adomet_syntD2; 1.
 DR Pfam: PF02773; S-Adomet_syntD3; 1.
 DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
 DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
 DR TRANSFERASE: One-carbon metabolism; Multigene family; ATP-binding.
 FT BINDING 119 124 ATP (POTENTIAL).
 FT BINDING 147 147 ATP (POTENTIAL).
 SQ SEQUENCE 390 AA; 42765 MW; F49DBEBE96605B CRC64;

alignment_scores:
 Quality: 101.00 Length: 24
 Ratio: 4.810 Gaps: 0
 Percent Similarity: 87.500 Percent Identity: 79.167

alignment_block:
 US-09-198-779B-1 x METK_PETHY ..

Align seg 1/1 to: METK_PETHY from: 1 to: 390

160 AGGTTTCATCAGACCGCGCATACGCCACTTGGCCGTGACGACGCCGA 209
 |||::: |||||
 361 ArgTyrGlnLysThrAlaIatYrGlyHisPheGlyArgAspAspProAs 377
 210 CTCACCTGCGAGGTGTCAG 231
 ||||| |||::: |||||
 377 pPheThrTrpGlnThrValLys 384

seq_name: SwissProt_40:METK_LYCES

seq_documentation_block:
 ID METK_LYCES STANDARD: PRT; 390 AA.
 AC P43282;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE S-adenosylmethionine synthetase 3 (EC 2.5.1.6) (Methionine
 adenosyltransferase 3) (Adomet synthetase 3).
 GN SAM3.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. Rutgers;
 RX MEDLINE=94289646; PubMed=8018871;
 RA Espartero J., Pintor-Toro J.A., Pardo J.M.;
 RT "Differential accumulation of S-adenosylmethionine synthetase
 transcripts in response to salt stress";
 RL Plant Mol. Biol. 25:217-227(1994).
 CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
 CC METHIONINE AND ATP.
 CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
 CC diphosphate + S-adenosyl-L-methionine.
 CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
 CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
 CC
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 CC
 CC EMBL: Z24743; CAA80867.1; -
 DR HSSP: P04384; 1MXB.
 DR InterPro: IPR002133; S-Adomet_synt.
 DR Pfam: PF00438; S-Adomet_synt; 1.
 DR Pfam: PF02772; S-Adomet_syntD2; 1.
 DR Pfam: PF02773; S-Adomet_syntD3; 1.

alignment_scores:
 Quality: 75.00 Length: 18
 Ratio: 4.688 Gaps: 0
 Percent Similarity: 88.889 Percent Identity: 72.222

alignment_block:

US-09-198-779B-1 x METK_RICTY

Align seg 1/1 to: METK_RICTY from: 1 to: 382

169 AAGACCCGCGATACGCCACTTGGCCGTGACGACGCCGACCTTCACCTG 218
 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 354 LysThrAlaSerTyrGlyHisPheGlyArgGluAspGluAsnPheThrTr 370

219 CGAG 222
 |||
 370 pGlu 371

seq_name: SwissProt_40:METK_RICPR

seq_documentation_block:

ID METK_RICPR STANDARD; PRT; 380 AA.

AC P56878;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine
 adenosyltransferase) (Adomet synthetase) (MAT).
 GN METK OR RP777.
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 OX NCBI_TaxID:782;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MADRID E;
 RX MEDLINE=99039499; PubMed=9823893;
 RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
 RA Sicheeritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeisund A.K.,
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 RT mitochondria.";
 RT Nature 396:133-140(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B;
 RX MEDLINE=99416441; PubMed=10486973;
 RA Andersson J.O., Andersson S.G.E.;
 RT Mol. Biol. Evol. 16:1178-1191(1999).
 DE "Genome degradation is an ongoing process in Rickettsia.";
 DE -1- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
 DE methionine and ATP. The overall synthetic reaction is composed of
 DE two sequential steps, Adomet formation and the subsequent
 DE triphosphosphate hydrolysis which occurs prior to release of
 DE Adomet from the enzyme (By similarity).
 DE -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
 DE dihydrophosphate + S-adenosyl-L-methionine.
 DE -1- COFACTOR: 2 divalent ions, such as magnesium, and 1 potassium ion
 DE bind per subunit (By similarity).
 DE -1- PATHWAY: Activated methyl cycle.
 DE -1- SUBUNIT: Homotrimer (By similarity).
 DE -1- SUBCELLULAR LOCATION: Cytoplasmic.
 DE -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
 DE -1- CAUTION: METK IS NON FUNCTIONAL IN STRAIN MADRID E WHOSE COMPLETE
 DE GENOME HAS BEEN SEQUENCED. IT IS INTERRUPTED BY A STOP CODON IN
 DE POSITION 141.

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DR EMBL: AJ235273; -; NOT ANNOTATED_CDS.
 DR EMBL: AJ238756; CAB56090.1; -.
 DR HSSP: P04384; 1MXB.
 DR InterPro: IPR002133; S-Adomet_synth.
 DR Pfam: PF00438; S-Adomet_synth; 1.
 DR Pfam: PF02772; S-Adomet_synth2; 1.
 DR Pfam: PF02773; S-Adomet_synth3; 1.
 DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
 DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
 KW Transferase, One-carbon metabolism, ATP-binding, Magnesium;
 KW Complete proteome.
 FT NP_BIND 260 267 APP (POTENTIAL).
 FT METAL 17 17 MAGNESIUM (BY SIMILARITY).
 FT METAL 272 272 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 380 AA: 42149 MW: DIB29BB64481FECA CRC64;

alignment_scores:
 Quality: 74.00 Length: 18
 Ratio: 4.625 Gaps: 0
 Percent Similarity: 88.889 Percent Identity: 72.222

alignment_block:

US-09-198-779B-1 x METK_RICPR

Align seg 1/1 to: METK_RICPR from: 1 to: 380

169 AAGACCCGCGATACGCCACTTGGCCGTGACGACGCCGACCTTCACCTG 218
 |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
 354 LysThrAlaSerTyrGlyHisPheGlyArgGluAspGluAsnPheThrTr 370

219 CGAG 222
 |||
 370 pGlu 371

seq_name: SwissProt_40:METK_THEMA

seq_documentation_block:

ID METK_THEMA STANDARD; PRT; 395 AA.

AC O9XIV8;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine
 adenosyltransferase) (Adomet synthetase) (MAT).
 GN METK OR TM1658.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogales; Thermotoga.
 OX NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSB8 / DSM 3109;
 RX MEDLINE=99287316; PubMed=10360571;
 RA Nelson K.E., Clayton R.A., Gail S.R., Gwin M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt W.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 RT genome sequence of Thermotoga maritima.";
 RT Nature 399:323-329(1999).
 DE -1- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
 DE methionine and ATP. The overall synthetic reaction is composed of
 DE two sequential steps, Adomet formation and the subsequent
 DE triphosphosphate hydrolysis which occurs prior to release of
 DE Adomet from the enzyme (By similarity).
 DE -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
 DE dihydrophosphate + S-adenosyl-L-methionine.

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```

CC -1- COFACTOR: 2 divalent ions, such as magnesium, and 1 potassium ion
CC bind per subunit (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AE001807; AAD36725.1; -.
CC DR HSSP: P04384; IMXB.
CC DR TIGR: TML658; -.
CC DR InterPro: IPR002133; S-Adomet_synth.
CC DR Pfam: PF00438; S-Adomet_synth2; 1.
CC DR Pfam: PF02772; S-Adomet_synth3; 1.
CC DR Pfam: PF02773; S-Adomet_synth3; 1.
CC DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
CC DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
CC KN Transferase: One-carbon metabolism; ATP-binding; Magnesium;
CC Complete proteome.
CC FM NP_BIND 270 277 ATP (POTENTIAL).
CC FT METAL 16 16 MAGNESIUM (BY SIMILARITY).
CC FT METAL 282 282 MAGNESIUM (BY SIMILARITY).
CC SQ SEQUENCE 395 AA; 43673 MW; 5ACA50F1DA60A9D5 CRC64;

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alignment_scores:
  Quality: 74.00      Length: 18
  Ratio: 4.625        Gaps: 0
  Percent Similarity: 88.889   Percent Identity: 72.222

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alignment_block:

US-09-198-779b-1 x METK_THEMA ..

Align seg 1/1 to: METK_THEMA from: 1 to: 395

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169 AAGACCGCGCATTACGGCCACTTTGGCCGTGACGACGCCGACCTTCACCTG 218
    |||||||
364 LysThrAlaIatYrGlyHisPheGlyArgAsnIuGluGluPheIrrTr 380
    219 CGAG 222
    |||
    380 pGIu 381

```

seq_name: SwissProt_40:METK_ACACA

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seq_documentation_block:
ID METK_ACACA STANDARD: PRT; 388 AA.
AC Q95032;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine
DE adenosyltransferase) (Adomet synthetase).
OS Acanthamoeba castellanii (Ameoba).
OC Eukaryota; Acanthamoebidae; Acanthamoeba.
OX NCBI_TaxID=5755;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97236447; PubMed=9116037;
RA Ahn K.S., Henney H.R. Jr.;
RT "Nucleotide sequence and developmental expression of Acanthamoeba
RT S-adenosylmethionine synthetase gene.";
RL Biochim. Biophys. Acta 1351:223-230(1997).
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +

```

```

CC diphosphate + S-adenosyl-L-methionine.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL: X79205; CAA55794.1; -.
CC DR HSSP: P04384; IMXB.
CC DR InterPro: IPR002133; S-Adomet_synth.
CC DR Pfam: PF00438; S-Adomet_synth; 1.
CC DR Pfam: PF02772; S-Adomet_synth2; 1.
CC DR Pfam: PF02773; S-Adomet_synth3; 1.
CC DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
CC DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
CC KN Transferase: One-carbon metabolism; ATP-binding.
CC FM NP_BIND 120 125 ATP (POTENTIAL).
CC SQ SEQUENCE 388 AA; 42617 MW; 7CA72AF37B2A4A08 CRC64;

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alignment_scores:
  Quality: 68.00      Length: 21
  Ratio: 4.250        Gaps: 0
  Percent Similarity: 76.190   Percent Identity: 61.905

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alignment_block:

US-09-198-779b-1 x METK_ACACA ..

Align seg 1/1 to: METK_ACACA from: 1 to: 388

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169 AAGACCGCGCATTACGGCCACTTTGGCCGTGACGACGCCGACCTTCACCTG 218
    |||||||
364 LysThrAlaIatYrHisGlyHisPheGlyArgAsnIuGluGluPheIrrTr 380
    219 CGAGTGTCTCAAG 231
    |||
    380 pGIuAlaProLys 384

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seq_name: SwissProt_40:METK_BACSU

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seq_documentation_block:
ID METK_BACSU STANDARD: PRT; 400 AA.
AC P54419; O34566;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine
DE adenosyltransferase) (Adomet synthetase) (MAT).
GN METK OR METE.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=168 / PY79;
RX MEDLINE=96345628; PubMed=8755891;
RA Yocum R., Perkins J.B., Howitt C.L., Pero J.;
RT "Cloning and characterization of the metE gene encoding S-
RT adenosylmethionine synthetase from Bacillus subtilis.";
RL J. Bacteriol. 178:4604-4610(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98048467; PubMed=9387221;
RA Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;
RT "Sequencing and functional annotation of the Bacillus subtilis genes
RT in the 200 kb trnB-dnaB region.";
RL Microbiology 143:3431-3441(1997).

```

```
CC -! FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP. The overall synthetic reaction is composed of
CC two sequential steps, Adomet formation and the subsequent
CC tripolysphosphate hydrolysis which occurs prior to release of
CC Adomet from the enzyme (By similarity).
CC -! CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -! COFACTOR: 2 divalent ions, such as magnesium, and 1 potassium ion
CC bind per subunit (By similarity).
CC -! PATHWAY: Activated methyl cycle.
CC -! SUBUNIT: Homotetramer (By similarity).
CC -! SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U52812; AAB17066.1; -
DR EMBL: AF008220; AAC00242.1; -
DR EMBL: Z99119; CAB15033.1; -
DR HSSP: P04384; IMXB.
DR Subtilist; Bg11840; metK.
DR Interpro: IPR002133; S-Adomet synt.
DR Pfam: PF00438; S-Adomet synt. 1.
DR Pfam: PF02772; S-Adomet syntd; 1.
DR Pfam: PF02773; S-Adomet syntd3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
DR Trnsferase; One-carbon metabolism; ATP-binding; Magnesium;
DR complete proteome.
FT NP_BIND 274 281 ATP (POTENTIAL).
FT METAL 19 19 MAGNESIUM (BY SIMILARITY).
FT METAL 286 286 MAGNESIUM (BY SIMILARITY).
FT CONFLICT 26 26 S -> Y (IN REF. 1).
FT CONFLICT 111 111 Q -> P (IN REF. 1).
FT CONFLICT 140 140 A -> V (IN REF. 1).
SQ SEQUENCE 400 AA; 44042 MW; EF3D97DCD375714A CRC64;

alignment_scores:
Quality: 65.00 Length: 18
Ratio: 4.333 Gaps: 0
Percent Similarity: 83.333 Percent Identity: 66.667

alignment_block:
US-09-198-779B-1 x METK_BACSU ..
Align seg 1/1 to: METK_BACSU from: 1 to: 400

169 AAGACGGCGGATAGCGGACCTTGGCGGTGACGAGCGGCGGACTTACCTG 218
:::|||||
368 GlnThrAlaIatYrGlyHisPheGlyArgHisAspValAspLeuProT 384
219 CGAG 222
|||
384 pglu 385

seq_name: SwissProt_40:METK_STRST
seq_documentation_block:
ID METK_STRST STANDARD; PRT; 411 AA.
AC 09X402;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine
DE adenosyltransferase) (Adomet synthetase) (MAT).
GN METK.
```

```
OS Streptomyces spectabilis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomyces; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=68270;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 27741.
RA Hyun C.G., Suh J.W.;
RT "Cloning of the gene for S-adenosyl-methionine synthetase from
RT Streptomyces spectabilis."
RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
CC -! FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP. The overall synthetic reaction is composed of
CC two sequential steps, Adomet formation and the subsequent
CC tripolysphosphate hydrolysis which occurs prior to release of
CC Adomet from the enzyme (By similarity).
CC -! CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -! COFACTOR: 2 divalent ions, such as magnesium, and 1 potassium ion
CC bind per subunit (By similarity).
CC -! PATHWAY: Activated methyl cycle.
CC -! SUBUNIT: Homotetramer (By similarity).
CC -! SUBCELLULAR LOCATION: Cytoplasmic.
CC -! SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF117274; AAD2464.1; -
DR HSSP: P04384; IMXB.
DR Interpro: IPR002133; S-Adomet synt.
DR Pfam: PF00438; S-Adomet synt. 1.
DR Pfam: PF02772; S-Adomet syntd; 1.
DR Pfam: PF02773; S-Adomet syntd3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
DR Trnsferase; One-carbon metabolism; ATP-binding; Magnesium.
FT NP_BIND 277 284
FT METAL 17 17 MAGNESIUM (BY SIMILARITY).
FT METAL 289 289 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 411 AA; 44658 MW; FC87DD5811CDB355 CRC64;

alignment_scores:
Quality: 64.00 Length: 20
Ratio: 4.000 Gaps: 0
Percent Similarity: 80.000 Percent Identity: 60.000

alignment_block:
US-09-198-779B-1 x METK_STRST ..
Align seg 1/1 to: METK_STRST from: 1 to: 411

163 TTCATGAGACCGCGGATAGCGGACCTTGGCGGTGACGAGCGGCGGACTT 212
:::|||||
369 TyrSerGlnThrAlaIatYrGlyHisPheGlyArgSerLeuProGluPh 385
213 CACGTGCGAG 222
|||||
385 ethrTpglu 388

seq_name: SwissProt_40:METK_HUMAN
seq_documentation_block:
ID METK_HUMAN STANDARD; PRT; 395 AA.
AC P31153;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
```

ID	METK_RAT	STANDARD;	PRT;	395 AA.
AC	P18296;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	15-JUL-1998 (Rel. 36, Last annotation update)			
DE	S-adenosylmethionine synthetase gamma form (EC 2.5.1.6) (Methionine			
DE	adenosyltransferase) (Adomet synthetase) (MAT-II).			
GN	MAT2A OR AMS2.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_Taxid=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=H12AR; TISSUE=Kidney;			
RX	MEDLINE=90337979; Pubmed=1696256;			
RA	Horiikawa S., Sasuga J., Shimizu K., Ozasa H., Tsukada K.;			
RT	"Molecular cloning and nucleotide sequence of cDNA encoding the rat			
RL	kidney S-adenosylmethionine synthetase.";			
RL	J. Biol. Chem. 265:13683-13686(1990).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Hiroki T., Horiikawa S., Tsukada K.;			
RL	Submitted (FEB-1997) to the EMBL/GenBank/DBP databases.			
CC	-1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM			
CC	METHIONINE AND ATP.			
CC	-1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +			
CC	diphosphate + S-adenosyl-L-methionine.			
CC	-1- PATHWAY: ACTIVATED METHYL CYCLE.			
CC	-1- SUBUNIT: HOMODIMER.			
CC	-1- TISSUE SPECIFICITY: IN MAMMALIAN TISSUES, THERE ARE THREE DISTINCT			
CC	FORMS OF ADOMET SYNTH. DESIGNATED AS ALPHA, BETA, AND GAMMA. ALPHA			
CC	AND BETA ARE EXPRESSED ONLY IN ADULT LIVER, WHILE GAMMA IS WIDELY			
CC	DISTRIBUTED IN EXTRAHEPATIC TISSUES. IN ADDITION THE GAMMA FORM			
CC	PREDOMINANTLY EXISTS IN FETAL RAT LIVER AND IS PROGRESSIVELY			
CC	REPLACED BY THE ALPHA AND BETA FORMS DURING DEVELOPMENT.			
CC	-1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.			
CC	-----			
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CC	CC entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	CC or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; J05571; AAA42106.1; -			
DR	EMBL; AB000717; BAA19170.1; -			
DR	EMBL; AB000716; BAA19170.1; JOINED.			
DR	PIR; A37118; A37118.			
DR	HSSP; P04384; IMXB.			
DR	InterPro: IPR002133; S-Adomet_synt.			
DR	Pfam; PF00438; S-Adomet_synt.1.			
DR	Pfam; PF02772; S-Adomet_synt2.1.			
DR	Pfam; PF02773; S-Adomet_synt3.1.			
DR	PROSITE; PS00376; ADOMET_SYNTHETASE.1; 1.			
DR	PROSITE; PS00377; ADOMET_SYNTHETASE.2; 1.			
KW	Transferase; One-carbon metabolism; Multigene family; ATP-binding.			
FT	NP_BIND 131 136 ATP (POTENTIAL).			
FT	BLINDING 159 159 ATP (POTENTIAL).			
SO	SEQUENCE 395 AA; 43715 MW; 4DA9AFABF7D09C79 CRC64;			
CC	-----			
CC	alignment_scores:			
CC	Quality: 63.00 Length: 21			
CC	Ratio: 3.938 Gaps: 1			
CC	Percent Similarity: 76.190 Percent Identity: 66.667			
CC	-----			
CC	alignment_block:			
CC	US-09-198-779B-1 x METK_RAT ..			
CC	Align seg 1/1 to METK_RAT from: 1 to: 395			


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CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U36379; AAA79506.1; -.
DR HSSP: P04384; IMXB.
DR InterPro: IPR002133; S-Adomet_synt.
DR Pfam: PF00438; S-Adomet_synt.1.
DR Pfam: PF02772; S-Adomet_synt2; 1.
DR Pfam: PF02773; S-Adomet_synt3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
DR Transferrase; One-carbon metabolism; ATP-binding; Magnesium.
KW NP_BIND 273 280 ATP (POTENTIAL)
FT METAL 19 19 MAGNESIUM (BY SIMILARITY).
FT METAL 285 285 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 397 AA; 43591 MW; 4D3E222FA04EB758 CRC64;

alignment_scores:
Quality: 61.00 Length: 18
Ratio: 4.357 Gaps: 0
Percent Similarity: 77.778 Percent Identity: 66.667

alignment_block:
US-09-198-779B-1 x METK_STPAU ..
Align seg 1/1 to: METK_STPAU from: 1 to: 397

169 AAGACCGCGCATACGGCCACTTTGGCCGTGACGACGCGACTTCACCTG 218
:::|||||
367 GlnThrAlaIalatyrglyHisPheGlyArgThrAspValGluLeuProtr 383
219 CGAG 222
|||
383 pglu 384

seq_name: SwissProt_40:METK_BACHD
seq_documentation_block:
ID METK_BACHD STANDARD; PRT; 399 AA.
AC O9K709;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (methionine
DE adenosyltransferase) (Adomet synthetase) (MAT).
GN METK OR BH3300.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Mieno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
"Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).
CC -1- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP. The overall synthetic reaction is composed of
```

```
CC two sequential steps, Adomet formation and the subsequent
CC triphosphate hydrolysis which occurs prior to release of
CC Adomet from the enzyme (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O -> phosphate +
CC diaphosphate + S-adenosyl-L-methionine.
CC -1- COFACTOR: 2 divalent ions, such as magnesium, and 1 potassium ion
CC bind per subunit (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF001518; BAB07019.1; -.
DR HSSP: P04384; LFUG.
DR InterPro: IPR002133; S-Adomet_synt.
DR Pfam: PF00438; S-Adomet_synt.1.
DR Pfam: PF02772; S-Adomet_synt2; 1.
DR Pfam: PF02773; S-Adomet_synt3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
DR Transferrase; One-carbon metabolism; ATP-binding; Magnesium;
KW Complete proteome.
KW NP_BIND 276 283 ATP (POTENTIAL).
FT METAL 21 21 MAGNESIUM (BY SIMILARITY).
FT METAL 288 288 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 399 AA; 43795 MW; 51C9A4DCEAD5329 CRC64;

alignment_scores:
Quality: 61.00 Length: 18
Ratio: 4.067 Gaps: 0
Percent Similarity: 83.333 Percent Identity: 61.111

alignment_block:
US-09-198-779B-1 x METK_BACHD ..
Align seg 1/1 to: METK_BACHD from: 1 to: 399

169 AAGACCGCGCATACGGCCACTTTGGCCGTGACGACGCGACTTCACCTG 218
:::|||||
370 GlnThrAlaIalatyrglyHisPheGlyArgThrAspValGluLeuProtr 386
219 CGAG 222
|||
386 pglu 387

seq_name: SwissProt_40:METK_LACIA
seq_documentation_block:
ID METK_LACIA STANDARD; PRT; 399 AA.
AC O9CE00;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (methionine
DE adenosyltransferase) (Adomet synthetase) (MAT).
GN METK OR L11902.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
```

CC Aciinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
CX NCBI_TaxID=1773;
[1]
RP SEQUENCE FROM N.A.
RC SRRAIN-H37RV;
RC MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Fellwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagsels K., Krogh A., Mclean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajadaram M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sluison J.E., Taylor K., Whitehead S., Barrell B.G.:
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence.";
RL Nature 393:537-544(1998).
[2]
RP SEQUENCE FROM N.A.
RC SRRAIN-CDC 1551 / Oshkosh;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
RA Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
RA Detmmer A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishal W.:
RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains.";
RL submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP. The overall synthetic reaction is composed of
CC two sequential steps, Adomet formation and the subsequent
CC tripolyphosphate hydrolysis which occurs prior to release of
CC Adomet from the enzyme (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC S-adenosyl-L-methionine.
CC -1- COFACTOR: 2 divalent ions, such as magnesium, and 1 potassium ion
CC bind per subunit (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.

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CC CC
DR EMBL; Z80108; CAB02194.1; -
DR EMBL; AE007015; AAA45702.1; ALT_INIT.
DR HSSP; P04384; IMXB.
DR TIGR; MT1437; -
DR TubercuList; RV1392; -
DR InterPro; IPR002133; S-Adomet_synth.
DR Pfam; PF00438; S-Adomet_synth; 1.
DR Pfam; PF02772; S-Adomet_synth; 1.
DR Pfam; PF02773; S-Adomet_synth; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
KW Transferase; One-carbon metabolism; ATP-binding; Magnesium;
KW Complete proteome.
FT NP-BIND 280 287 ATP (POTENTIAL).
FT METAL 19 19 MAGNESIUM (BY SIMILARITY).
FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 403 AA; 43046 MW; 2E18BE05D8267972 CRC64;

Alignment_scores:
Quality: 61.00 Length: 20
Ratio: 4.067 Gaps: 0
Percent Similarity: 75.000 Percent Identity: 55.000

alignment_block:

US-09-198-779B-1 x METK_MYCTU ..

Align seg 1/1 to: METK_MYCTU from: 1 to: 403

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163 TTTCATCAAGACCGCATACGGCCACTTTGGCGGTGACGACGCGACTT 212
    ::::::::::::::::::::::::::::::::::::::::::::
372 TTTATLAPROTTHALALATATYRGLYHISPhcGLYRTHRASVALGLULe 388
213 CACCTGGGAG 222
    ::::
388 UPROTTPGLU 391

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seq_name: SwissProt_40:METK_SYNY3

seq_documentation_block:

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ID METK_SYNY3 STANDARD; PRT; 426 AA.
AC P72871;
DT 15-DEC-1998 (Rel. 37, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine
DE adenosyltransferase) (Adomet synthetase) (MAT).
GN METK OR SL0927.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905221;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugijura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nairuo K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -1- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP. The overall synthetic reaction is composed of
CC two sequential steps, Adomet formation and the subsequent
CC triphosphosphate hydrolysis which occurs prior to release of
CC Adomet from the enzyme (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -1- COFACTOR: 2 divalent ions, such as magnesium, and 1 potassium ion
CC bind per subunit (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL: D90901; BAA16887.1; ALT_INIT.
DR HSSP: P04384; IMXB.
DR InterPro: IPR002133; S-Adomet_synth.
DR Pfam: PF00438; S-Adomet_synth; 1.
DR Pfam: PF02772; S-Adomet_synth2; 1.
DR Pfam: PF02773; S-Adomet_synth3; 1.
DR PROSITE: PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE: PS00377; ADOMET_SYNTHETASE_2; 1.
KW Transferase; One-carbon metabolism; ATP-binding; Magnesium;
KW Complete proteome.
FT NP_BIND 287 294 ATP (POTENTIAL).

```

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FT METAL 24 24 MAGNESIUM (BY SIMILARITY).
FT METAL 299 299 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 426 AA; 45865 MM; 0DFEBB5785F15FA CRC64;

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alignment_scores:

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Quality: 60.50 Length: 22
Ratio: 3.559 Gaps: 1
Percent Similarity: 77.273 Percent Identity: 59.091

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alignment_block:

US-09-198-779B-1 x METK_SYNY3 ..

Align seg 1/1 to: METK_SYNY3 from: 1 to: 426

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160 AGGTTTCATCAAG...ACCGCGCATACGGCCACTTTGGCGGTGACGACGC 206
    ::::::::::::::::::::::::::::::::::::::::::::
384 ArpghetyrglnAspValAlaAlaTyrGLYHISPhcGLYRTHRASpAspLe 400
207 CGACTTCACCTGGGAG 222
    ::::
400 uAspLeuPROTPGLU 405

```

seq_name: SwissProt_40:METK_TREPA

seq_documentation_block:

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ID METK_TREPA STANDARD; PRT; 396 AA.
AC O83772;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine
DE adenosyltransferase) (Adomet synthetase) (MAT).
GN METK OR TP0794.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NICHOLS;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.P., Weinstein G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalaf H., Richardson D., Howell J.K., Chidambaram M., Uteback T.,
RA McDonald L., Artlisch P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete.";
RL Science 281:375-388(1998).
CC -1- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP. The overall synthetic reaction is composed of
CC two sequential steps, Adomet formation and the subsequent
CC triphosphosphate hydrolysis which occurs prior to release of
CC Adomet from the enzyme (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -1- COFACTOR: 2 divalent ions, such as magnesium, and 1 potassium ion
CC bind per subunit (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC -----

```



```

DR EMBL; AED01250; AAC65758.1; -
DR HSSP; P04384; IMXB.
DR TIGR; TP0794; -
DR InterPro; IPR002133; S-Adomet_synth.
DR Pfam; PF00438; S-Adomet_synth; 1.
DR Pfam; PF02772; S-Adomet_synth2; 1.
DR Pfam; PF02773; S-Adomet_synth3; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
DR Transferrase; One-carbon metabolism; ATP-binding; Magnesium;
KM complete proteome.
FT NE_BIND 264 271 ATP (POTENTIAL).
FT METAL 16 16 MAGNESIUM (BY SIMILARITY).
FT METAL 276 276 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 396 AA; 42990 MW; E532DD39B0BBE711 CRC64;

alignment_scores:
Quality: 59.00 Length: 33
Ratio: 2.565 Gaps: 2
Percent Similarity: 69.697 Percent Identity: 39.394

alignment_block:
US-09-198-779B-1 x METK_TREPA ..
Align seg 1/1 to: METK_TREPA from: 1 to: 396

160 AGCTTCATCAGACCGCGCATACGCGCATTTGGCGCTGACGAC..... 204
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
355 ArgYrArGserThAlaValrGlYhIsPhgIyArGluGlNpHePr 371
205 .....GCCGACTTCACCTCGCGAGTG.....GTCAAGCCC 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
371 cTpeLnaRgYhRAspYsAlaGAspLeuGlNaRgAlaValaRgPro 387

seq_name: SwissProt_40:METL_RAT

seq_documentation_block:
ID METL_RAT STANDARD; PRT; 397 AA.
AC P13444;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE S-adenosylmethionine synthetase alpha and beta forms (EC 2.5.1.6)
DE (Methionine adenosyltransferase) (Adomet synthetase) (MAT-I/III).
DE MATIa OR AMSI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=Liver;
RX MEDLINE=90032633; PubMed=2806235;
RA Horikawa S., Ishikawa M., Ozasa H., Tsukada K.;
RT "Isolation of a cDNA encoding the rat liver S-adenosylmethionine
synthetase.";
RL Eur. J. Biochem. 184:497-501(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA Mato J.M.;
RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
METHIONINE AND ATP.
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
diphosphate + S-adenosyl-L-methionine.
CC -!- PATHWAY: ACTIVATED METHYL CYCLE.
CC -!- SUBUNIT: HOMOTETRAMER FOR THE ALPHA FORM (MAT-I); HOMODIMER FOR
THE BETA FORM (MAT-III).
CC -!- TISSUE SPECIFICITY: IN MAMMALIAN TISSUES, THERE ARE THREE DISTINCT
FORMS OF ADOMET SYNTH. DESIGNATED AS ALPHA, BETA, AND GAMMA. ALPHA
AND BETA ARE EXPRESSED ONLY IN ADULT LIVER, WHILE GAMMA IS WIDELY
DISTRIBUTED IN EXTRAHEPATIC TISSUES. IN ADDITION THE GAMMA FORM

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CC CC PREDOMINANTLY EXISTS IN FETAL RAT LIVER AND IS PROGRESSIVELY
CC REPLACED BY THE ALPHA AND BETA FORMS DURING DEVELOPMENT.
CC -!- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X15734; CA33754.1; -
DR EMBL; X60822; -; NOT_ANNOTATED_CDS.
DR PIR; S06114; S06114.
DR PIR; S18256; S18256.
DR HSSP; P04384; IMXB.
DR InterPro; IPR002133; S-Adomet_synth.
DR Pfam; PF00438; S-Adomet_synth; 1.
DR Pfam; PF02772; S-Adomet_synth2; 1.
DR Pfam; PF02773; S-Adomet_synth3; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
DR Transferrase; One-carbon metabolism; Multiligene family; ATP-binding.
FT NP_BIND 132 137 ATP (POTENTIAL).
FT BINDING 160 160 ATP (POTENTIAL).
SQ SEQUENCE 397 AA; 43698 MW; AB47A8CCBB2007BA CRC64;

alignment_scores:
Quality: 59.00 Length: 21
Ratio: 3.688 Gaps: 1
Percent Similarity: 76.190 Percent Identity: 61.905

alignment_block:
US-09-198-779B-1 x METL_RAT ..
Align seg 1/1 to: METL_RAT from: 1 to: 397

169 AAGACCGCGCGCATACGCGCATTTGGCGTGAAGCGCGACTTCACGCG 218
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
375 LysThAlaGysTrGlYhIsPhgIyArG.....SerGlupHeProTr 389
219 CGAGTGCGTCAAG 231
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
389 pEluValProLys 393

seq_name: SwissProt_40:METK_BUCAI

seq_documentation_block:
ID METK_BUCAI STANDARD; PRT; 378 AA.
AC P57486;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine
adenosyltransferase) (Adomet synthetase) (MAT).
GN METK OR BU408.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TOKYO 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Matanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. Aps.";
RL Nature 407:81-86(2000).
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
methionine and ATP. The overall synthetic reaction is composed of
two sequential steps, Adomet formation and the subsequent

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CC tripolyphosphate hydrolysis which occurs prior to release of
CC AdoMet from the enzyme (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -1- COFACTOR: 2 divalent ions, such as magnesium, and 1 potassium ion
CC bind per subunit (By similarity).
CC -1- PATHWAY: Activated methyl cycle.
CC -1- SUBUNIT: Homotrimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AP001119; BAB13109.1; -.
CC InterPro: IPR002133; S-AdoMet_synth.
CC Pfam: PF00438; S-AdoMet_synth2; 1.
CC Pfam: PF02772; S-AdoMet_synth2; 1.
CC Pfam: PF02773; S-AdoMet_synth2; 1.
CC PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
CC PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
CC Transferrase; One-carbon metabolism; ATP-binding; Magnesium;
CC Complete proteome.
CC NP_BIND 260 267 ATP (POTENTIAL).
CC METAL 17 17 MAGNESIUM (BY SIMILARITY).
CC METAL 272 272 MAGNESIUM (BY SIMILARITY).
CC SEQUENCE 378 AA; 41706 MW; C2C12B90561B71C8 CRC64;

alignment_scores:
    Quality: 58.00      Length: 14
    Ratio: 4.462      Gaps: 0
    Percent Similarity: 92.857      Percent Identity: 64.286

alignment_block:
US-09-198-779B-1 x METK_BUCAI ..
Align seg 1/1 to: METK_BUCAI from: 1 to: 378

163 TTCATCAAGACCGCGCATACGGCCATTGGCGGTGACGAC 204
      ::::::::::::::::::::::::::::::::::::
352 TyrleuLysThrAlaValTyrGlyHisheGlyArgLysGlu 365

seq_name: SwissProt_40:POLN_SOUV3

seq_documentation_block:
ID POLN_SOUV3 STANDARD; PRT; 1788 AA.
AC 004544;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Non-structural polyprotein [Contains: RNA-directed RNA polymerase
DE (EC 2.7.7.48); Thiol protease (EC 3.4.22.-); Helicase (2C like
DE protein)].
OS Southampton virus (serotype 3).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Norwalk-like viruses.
OX NCBL_TaxID=37129;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93142023; PubMed=8380940;
RA Lambden P.R., Caud E.O., Ashley C.R., Clarke I.N.;
RT "Sequence and genome organization of a human small round-structured
RT (Norwalk-like) virus."
RL Science 259:516-519(1993).
RN [2]
RN REVISIONS.
RX MEDLINE=96088083; PubMed=8560774;
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RA Lambden P.R., Liu B., Clarke I.N.;
RT "A conserved sequence motif at the 5' terminus of the Southampton
RT virus genome is characteristic of the Caliciviridae."
RL Virus Genes 10:149-152(1995).
CC -1- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY C37.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L07418; AAA92983.1; -.
CC PIR; A37491; A37491.
CC MEROPS: C37.001; -.
CC InterPro: IPR004004; Calici_pol_hel.
CC InterPro: IPR000605; RNA_helicase.
CC InterPro: IPR001205; RNA_pol_p3d.
CC Pfam: PF00680; RNA_dep_cysptase.
CC Pfam: PF00910; RNA_helicase; 1.
CC PRINTS; PR00918; CALICIVIRUS.
CC PRINTS; PR00917; SRSVCYSPASE.
CC Polyprotein; Transferrase; RNA-directed RNA polymerase; Hydrolase;
CC Thiol protease; Helicase; ATP-binding.
CC CHAIN ? ? HELICASE (P2C-LIKE).
CC FT CHAIN 714 1319
CC FT NP_BIND 561 568
CC FT ACT_SITE 1236 1238
CC FT ACT_SITE 1236 1256
CC FT ACT_SITE 1236 1256
CC SEQUENCE 1788 AA; 198581 MW; 9EDA4F6529793652F CRC64;

alignment_scores:
    Quality: 57.50      Length: 55
    Ratio: 2.130      Gaps: 2
    Percent Similarity: 49.091      Percent Identity: 27.273

alignment_block:
US-09-198-779B-1/rev x POLN_SOUV3 ..
Align seg 1/1 to: POLN_SOUV3 from: 1 to: 1788

230 TTGACCACTCGCAGGTGAAGTGGCGGTGTCACGGCAAGTGGCGTA 181
      ::::::::::::::::::::::::::::
253 LeuSerTyrAspGlnLeuLysGlnLeuGlnAsnGluPro...TriProTyr 268

180 TGGCGCGGTCTGTGATGACCTGNNNNNNNNNNNNNNNNNNNNNNNN 131
      ::::::::::::::::::::
268 rAlaAlaIleThrAsnAsnCys..... 275

130 NNNNNNNNAAGTACGCTGTTGTCGCTGCTCATATATACACATTATA 81
      ::::::::::::::::::::
276 .....PheGluPheCysGlnValMetCysLeuGlnAspThrTrp 289

80 ACACAACGAACAATG 66
      ::::::::::
290 LeuGlnArgArgLeu 294

seq_name: SwissProt_40:CLT2_HUMAN

seq_documentation_block:
ID CLT2_HUMAN STANDARD; PRT; 346 AA.
AC 09NS75; 09HC02;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cysteineyl leukotriene receptor 2 (CysLTR2) (P5ECO146) (HG57) (HPN321).
DE CysLTR2 OR CysLTR2 OR CysLTR2.
OS Homo sapiens (Human).
OX Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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KR PROSITE: PS50262; G_PROTEIN_RECP_F1.2; 1.
RM G-protein coupled receptor; Transmembrane: Glycoprotein.
FT DOMAIN 1 42 42 1 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 43 63 63 1 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 64 72 72 2 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 73 93 93 2 (POTENTIAL).
FT DOMAIN 94 123 123 3 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 124 144 144 3 (POTENTIAL).
FT DOMAIN 145 153 153 4 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 154 174 174 4 (POTENTIAL).
FT DOMAIN 175 204 204 5 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 205 225 225 5 (POTENTIAL).
FT DOMAIN 226 245 245 6 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 246 266 266 6 (POTENTIAL).
FT DOMAIN 267 286 286 7 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 287 307 307 7 (POTENTIAL).
FT DOMAIN 308 346 346 7 CYTOPLASMIC (POTENTIAL).
FT DISULFID 111 187 187 BY SIMILARITY.
FT CARBOHYD 20 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 26 26 26 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 30 30 30 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 181 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 346 AA; 39635 MW; EB54A4A2DDCE5EE4 CRC64;

alignment_scores:
Quality: 57.00 Length: 18
Ratio: 3.800 Gaps: 0
Percent Similarity: 83.333 Percent Identity: 50.000

alignment_block:
US-09-198-779B-1/rev x CLR2_HUMAN ..

Align seg 1/1 to: CLR2_HUMAN from: 1 to: 346

64 ATCAGGACCGTCATTTATCAAGCATGGGACGCGATCTGCCACCGAG 15
:::||||| ||||| ::::::||| :||||| |
266 LeuArgThrValHisLeuThrThrTrpLysValIglyLeucCysLysAspAr 282
14 GCTA 11
|||
282 gieu 283

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